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GenCore version 5.1.9
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ecember 31, 2006, 12:26:03 ; Search time 132.37 Seconds	(without alignments)
December 31, 20	
Run on:	

		updates/sec	
0.101	(without alignments)	6266.684 Miliion cell updates/sec	
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US-09-232-880-67 385 Title: Perfect score:

3050214 seqs, 1077301958 residues

Searched:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Published_Applications_NA_New:*	<pre>1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_NEW_PUB.seq:*</pre>	2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*	3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq:*	4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*	5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq:*	6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*	8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq1:*	9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq2:*	10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq3:*	<pre>11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq:*</pre>	
Database :											

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			di			SUMMARIES	
Res	Result No.	Score	Query	Query Match Length DB	DB	ID	Description
1						* * * * * * * * * * * * * * * * * * * *	
	-	385	100.0	385	7	US-11-344-932-67	Sequence 67, Appl
	~	385	100.0	385	10	US-11-349-541-67	Sequence 67, Appl
	m	307.2	79.8	3228	7	US-11-344-932-701	Sequence 701, App
υ	4	231.8	60.2	1016	80	US-11-266-748A-350613	Sequence 350613,
U	S	231.8	60.2	1016	8	US-11-266-748A-383047	Sequence 383047,
	9	231.8	60.2	1016	80	US-11-266-748A-433992	Sequence 433992,
	7	107.4	27.9	2841	7	US-11-344-932-700	Sequence 700, App
	œ	95	24.7	1016	80	US-11-266-748A-350613	Sequence 350613,
	σ	95	24.7	1016	œ	US-11-266-748A-383047	Sequence 383047,
U	10	95	24.7	1016	œ	US-11-266-748A-433992	Sequence 433992,
	11	89.2	23.2	5449	80	US-11-266-748A-32477	Sequence 32477, A
υ	12	84	21.8	385	7	US-11-344-932-67	Sequence 67, Appl
υ	13	84	21.8	385	10	US-11-349-541-67	Sequence 67, Appl
υ	14	77.2	20.1	25694	9	US-10-669-920-46	Sequence 46, Appl
υ	15	75.2	19.5	154394	ω	US-11-266-748A-58517	Sequence 58517, A
	16	73.8	19.2	80988	9	US-10-669-920-261	Sequence 261, App
υ	17	73.8	19.2	421987	60	US-11-266-748A-28210	Sequence 28210, A
ပ	18	70.4	18.3	3228	7	US-11-344-932-701	Sequence 701, App
υ	13	9.69	18.1		80	US-11-266-748A-254460	Sequence 254460,
	20	9.69	18.1	593	8	US-11-266-748A-314977	Sequence 314977,
	21	67.6	17.6	198285	œ	US-11-266-748A-59857	Sequence 59857, A
υ	22	9.79	17.6	4647455	9	US-10-641-321-205	Sequence 205, App

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11185, 29045,	• •	11257,	57638,	700, A	29041,	22664,	60144,	196189,	1613,	24171,	29041	11257,	57638,	28210,		1151, 7	203066,	699, A	32477, A	22, AI	4, App.
Sequence	Sequence	Seguence	Sequence	Sequence 700, App	Sequence 29041,	Sequence 22664,	Sequence 60144,	Sequence 196189,	Sequence 1613	Sequence 24171	Sequence 29041,	Sequence 11257,	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence 699, App	Sequence	Sequence 22, App	Sequence 4, Appli
US-11-371-354-11185 US-11-266-748A-29045	US-11-266-748A-200795	US-11-371-354-11257	US-11-266-748A-57638	US-11-344-932-700	US-11-266-748A-29041	US-11-266-748A-22664	US-11-266-748A-60144	US-11-266-748A-196189	US-11-073-360-1613	US-11-266-748A-24171	US-11-266-748A-29041	US-11-371-354-11257	US-11-266-748A-57638	US-11-266-748A-28210	US-10-669-920-1140	US-10-669-920-1151	US-11-266-748A-203066	US-11-344-932-699	US-11-266-748A-32477	US-11-330-648-22	US-10-669-920-4
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64.2	62.6	62.6	62.6	9	59.2	59	58.8	53.2	53	52	51.6	50.2	50.2	49.8	49.4	49.4	48.4	48	48	47.4	47.4
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ALIGNMENTS

RESULT 1

US-11-344-932-67	; Publication No. US20060269532A1	; GENERAL INFORMATION:	: Xu, Jiangchun	 	••	: Jiang, Yuqiu	: Henderson, Robe	: Kalos, N	: Fanger, Gary	: Retter,	: Stolk	: Day, Craig H.	: Vedvick,	<u>.</u>	 : Wang, Aijun	: Skeiky,	 : Hural, John	: McNeill, F	: Houghton, Raymond L.	٠	 : Watanabe, Yoshihir	: Meaghe	OF INVENTION: (; FILE REFERENCE: 210121.427C32	z	APPLICATION N	50-	; PRIOR FILING DATE: 2001-12-10 ·	APPLICATION N	FILING DATE: 2001-06-29	APPLICATION N	; PRIOR FILLING DATE: ZOUL-US-US	PITING DATE: 2001-02	FILLING DAILE:

¹ actacacacactccacttgc......tttctgtgctagtggaccgt 385 Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

⁶¹⁰⁰⁴²⁸ Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

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Foy, Teresa M
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                                                                                      TYPE: DNA ORGANISM: Homo sapien
                                                                                                                          US-11-349-541-67
                                                                       LENGTH: 385
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Sequence 67, Application US/11349541

Sequence 67, Application WS.0060223129A1

GENERAL INCORMATION:

APPLICANT: Xu, Jiangchun

APPLICANT: Dillon, Davin C.

TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND

TITLE OF INVENTION: METHODS FOR THEIR USE

FILE REPERBENCE: 210121.428C7

CURRENT APPLICATION NUMBER: US/11/349,541

CURRENT APPLICATION NUMBER: US 09/116,134

PRIOR APPLICATION NUMBER: US 09/020,66

PRIOR PILING DATE: 1998-07-14

PRIOR FILING DATE: 1998-02-25

PRIOR PILING DATE: 1998-02-25

PRIOR APPLICATION NUMBER: US 09/020,747

PRIOR APPLICATION NUMBER: US 08/04,809

PRIOR FILING DATE: 1997-08-01

PRIOR APPLICATION NUMBER: US 08/806,596
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100.0%; Score 385; DB 7; L
Best Local Similarity 100.0%; Pred. No. 2.9e-119;
Matches 385; Conservative 0; Mismatches 0;
             PRIOR PILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: 09/709,729
PRIOR FILING DATE: 2000-11-09
PRIOR FILING DATE: 2000-11-09
PRIOR PILING DATE: 2000-10-10
PRIOR APPLICATION NUMBER: 09/679,426
PRIOR APPLICATION NUMBER: 09/679,426
PRIOR PILING DATE: 2000-10-02
PRIOR FILING DATE: 2000-10-02
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-06
NUMBER OF SEQ ID NOS: 1033
SOFTWARE: PASCESQ for Windows Version 3.0
SOFTWARE: PASCESQ for Windows Version 3.0
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US-11-344-932-67
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US-11-349-541-67
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APPLICANT: Meagher, Madeleine Joy
APPLICANT: Deng, Ta
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
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                                                                                                                                                                                                                                                  Length 385;
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PRIOR FILING DATE: 1997-02-25
NUMBER OF SEQ ID NOS: 228
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 67
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McNeill, Patricia D.
Houghton, Raymond L.
Vinals y de Bassols, Carlota
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Henderson, Robert A.
APPLICANT: Ralos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
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Hepler, William T.
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Vedvick, Thomas S.
Carter, Darrick
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Publication No. US20060134663A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 7; Length 3228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 79.8%; Score 307.2; DB 7; Best Local Similarity 92.0%; Pred. No. 1.4e-92; Matches 346; Conservative 0; Mismatches 28;
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
     NAME/KEY: misc_feature
i_CCATION: 66, 2343, 2387, 3065
i_CTHER INFORMATION: n = A,T,C or G
US-11-344-932-701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         370 TGTGCTAGTGGACCGT 385
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                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
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442 CTCCACGTGCCTTTGTGAGATACTTTATCCCAGCACTTTAGGAATGCTAAGTTCAGATCA 383
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GENERAL INFORMATION:

APPLICANT: Johnston, Patrick
TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 5815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2004-11-03
PRIOR PELING DATE: 2004-11-03
PRIOR PELING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.9
PRIOR PELING DATE: 2004-11-03
PRIOR PELING DATE: 2005-01-18
PRIOR FILING DATE: 2005-03-18
PRIOR P
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88.0%; Pred. No. 1.9e-67;
tive 0; Mismatches 32;
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LOCATION: (954). (972)
OTHER INFORMATION: n is a, c,
US-11-266-7488-350613
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Best Local Similarity 88.0°
Matches 265; Conservative
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ORGANISM: Homo Sapiens
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LOCATION: (880)..(881)
OTHER INFORMATION: n is
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RESULT 5 US-11-266-748A-383047/c

RESULT 4 US-11-266-748A-350613/c ; Sequence 350613, Application US/11266748A

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      262 CGGGGGTTCACTTTTGAGACAGTTCTCCTCTGAGACCTGATCTCT----GCTGGGCAGTC 207
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Sequence 383047, Application US/11266748A
Publication No. US20060134663A1
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Harkin, Paul
APPLICANT: Harkin, Paul
APPLICANT: Mulligan, Kari
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: Methods of Using the Same
CURRENT FILING DATE: 2004-11-03
PRIOR PELING DATE: 2005-03-14
PRIOR PELING DATE: 2005-03-14
PRIOR PELING DATE: 2005-03-14
PRIOR PELING DATE: 2005-03-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | NAME/KEY: misc_feature
| LOCATION: (964).. (972)
| OTHER INFORMATION: n is a, c, g, or t
US-11-266-7488-383047
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OTHER INFORMATION: n is a,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           754
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 CTCCACTTGCCCTTGTGAGACACTTTGTCCCAGCACTTTAGGAATGCTGAGGTCGGACCA
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                                                                                                  STREAKL INVERFATION:

JOHNSTON TO ADDISTON, PALLICK
APPLICANT: Johnston, Patrick
APPLICANT: MULLIGAN, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REPRENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
FRIOR APPLICATION NUMBER: EP 04105492.6
FRIOR APPLICATION NUMBER: EP 04105482.6
FRIOR APPLICATION NUMBER: EP 04105483.4
FRIOR APPLICATION NUMBER: EP 04105483.9
FRIOR PILING DATE: 2004-11-03
FRIOR PELLING DATE: 2004-11-03
FRIOR FILING DATE: 2004-11-03
FRIOR FILING DATE: 2005-03-14
FRIOR FRIOR FILING DATE: 2005-03-14
FRIOR F
Sequence 433992, Application US/11266748A, Publication No. US20060134663A1, GENERAL INFORMATION:
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LOCATION: (45)...(53)
OTHER INFORMATION: n is a,
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ORGANISM: Homo Sapiens
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Best Local
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1364 CAGGGCACTCTCAGATGCCCATACTTTCTGTGCTAGTGGACCGT 1412
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APPLICANT: Johnston, Patrick
APPLICANT: Johnston, Patrick
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
VURRENT FILING DATE: 2005-11-03
PRIOR PELLING DATE: 2005-11-03
PRIOR PELLING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR PILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
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PRIOR FILING DATE: 2005-03-14
PRIOR PILING DATE: 2005-03-14
PRIOR PILING DATE: 2005-03-14
PRIOR PILING DATE: 2005-03-14
                                                                                337 CAGGGCACTCTCAGATGCCCATACCATAGTTTCTGTGCTAGTGGACCGT
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Pred. No. 2.2e-21;
0; Mismatches 80; Indels
                                                                                                                                                                                                                                                            Sequence 350613, Application US/11266748A Publication No. US20060134663A1 GENERAL INFORMATION:
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Best Local Similarity 65.1%;
Matches 157; Conservative (
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; LOCATION: (964)..(972)
; OTHER INFORMATION: n is a,
US-11-266-748A-350613
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LOCATION: (880)..(881)
OTHER INFORMATION: n is
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ORGANISM: Homo Sapiens
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NUMBER OF SEO ID NOS: 1033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 2841;
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CURRENT APPLICATION NUMBER: US/11/344,932
CURRENT FILING DATE: 2006-02-01
PRIOR PPLICATION NUMBER: 10/144,678
PRIOR FILING DATE: 2002-05-09
PRIOR APPLICATION NUMBER: 10/012,896
PRIOR APPLICATION NUMBER: 09/895,814
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SOFTWARE: FastSEQ for Windows Version 3.0
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Houghton, Raymond L.
Vinals y de Bassols, Carlota
Foy, Teresa M.
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PRIOR APPLICATION NUMBER: 09/759,143
PRIOR PILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: 09/709,729
PRIOR PILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: 09/685,166
PRIOR APPLICATION NUMBER: 09/695,166
PRIOR APPLICATION NUMBER: 09/679,426
PRIOR FILING DATE: 2000-10-02
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: 09/679,426
                                                    Application US/11344932
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PRIOR APPLICATION NUMBER: 09/852,911
PRIOR FILING DATE: 2001-05-09
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Meagher, Madeleine Joy
Deng, Ta
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US-11-344-932-700
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
                                                                                                                                                                                                                                      Jiang, Yuqiu
Henderson, Robert A.
Kalos, Michael D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Skeiky, Yasir A. W.
Hepler, William T.
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Vedvick, Thomas S.
Carter, Darrick
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Best Local Similarity 99.14
Matches 108; Conservative
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Retter, Marc W.
                                                                                                                                                                                                                                                                                                                                                                           John A.
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ORGANISM: Homo sapiens
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169 GGAGTGCTGATATCAGACCAGCCCCATCTCATGTGCAGGACTGCCCAGCAGAGATCAGGT 228 CTGAGAGTICCCCTTTTAAAAAGGGGACTTGCTTAAAAAAGAAGTCTAGCCACGATTGT 170 229 cricadadeagaachercraaaadreaacccceeeacacacaraderecrrracacaaac 288 171 GTAGAGCAGCTGTGCTGCAGATTCACTTTTGAGAGAGTTCTCCTCTGAGACCTGA 230 231 TCTTTAGAGGCTGGGCAGTCTTGCACATGAGATGGGGCTGGTCTGATCTCAGCACTCCTT 290 51 GGAATGCTGAGGTCGGACCAGCTCTCATGTGCAAGATTGCCCAGCAGACATCAGGT Gaps Length 1016; ઠ

0; Mismatches

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NAME/KEY: misc_feature
LOCATION: (135). (137)
OTHER INFORMATION: n is a, c,
US-11-266-748A-433992
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OTHER INFORMATION: n is a,
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                                                                                  JS-11-266-748A-433992/c
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                                                                                                                                                                                                                                               ### PUBLICANT: Harkin, Paul
### APPLICANT: Harberiptome Microarray Technology and
### APPLICANT: Harberiptom: Karl
### TITLE OF INVENTION: Methods of Using the Same
### PILE REFERENCE: 55815-0102 (319189)
### CURRENT APPLICATION NUMBER: US 04105479.2
### PRIOR PILING DATE: 2004-11-03
### PRIOR PILING DATE: 2005-03-14
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                                                                                                                                                                                                  Sequence 383047, Application US/11266748A
Publication No. US20060134663A1
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LOCATION: (964)...(972)
CTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-383047
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SOFTWARE: PatentIn version 3.3
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OTHER INFORMATION: n is a,
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Best Local Similarity 65.1
Matches 157; Conservative
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291 A 291
                                                         A 405
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LENGTH: 1016
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111 CTGAGAGTTCCCCTTTTAAAAAGGGGACTTGCTTAAAAAAGAAGTCTAGCCACGATTGT 170
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                                                                                                                                 APPLICANT: Harkin, Paul
APPLICANT: Hounston, Patrick
APPLICANT: Aulligan, Karl
APPLICANT: Mulligan, Karl
APPLICANT: Mulligan, Karl
ITIEE OF INVENTION: Transcriptome Microarray Technology and
TITIE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
GURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105492.6
PRIOR APPLICATION NUMBER: EP 04105403.4
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR PRILING DATE: 2004-11-03
PRIOR PRILING DATE: 2004-11-03
PRIOR PELING DATE: 2004-11-03
PRIOR FILING DATE: 2005-01-14
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-07-18
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24.7%; Score 95; DB 8; I
Best Local Similarity 65.1%; Pred. No. 2.2e-21;
Matches 157; Conservative 0; Mismatches 80;
Sequence 433992, Application US/11266748A Publication No. US20060134663A1 GENERAL INFORMATION:
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48 TTAGGAATGCTGAGGTCGGACCAGCCACATCTCATGTGCAAGATTGCCCAGC----AGAC 103
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                                                                                                                                                                                                                          APPLICANT: Deng, TA
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSIATE CANCER
FILE REFERENCE: 210121.427632
CURRENT APPLICATION NMBER: US/11/344,932
CURRENT FILING DATE: 2006-02-01
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                                                                     MCNEIL, Patricia D.
Houghton, Raymond L.
Vinals y de Bassols, Carlota
                                                                                                                                                                                                                                                                                                                                                                  CURRENT FILING DATE: 2006-02-01
PRIOR PEDICATION NUMBER: 10/144,678
PRIOR PELICATION NUMBER: 10/1012,896
PRIOR APPLICATION NUMBER: 10/012,896
PRIOR PILING DATE: 2001-12-10
PRIOR PELICATION NUMBER: 09/895,814
PRIOR PELING DATE: 2001-06-29
PRIOR PELING DATE: 2001-06-09
PRIOR PELING DATE: 2001-05-09
PRIOR PELING DATE: 2001-05-09
PRIOR PELING DATE: 2001-01-12
PRIOR PELING DATE: 2001-01-12
PRIOR PELING DATE: 2001-01-12
PRIOR PELING DATE: 2000-11-09
PRIOR PELING DATE: 2000-11-09
PRIOR PELING DATE: 2000-11-09
PRIOR PELING DATE: 2000-11-09
PRIOR PELING DATE: 2000-10-10
PRIOR PELING DATE: 2000-10-10
PRIOR PELING DATE: 2000-10-09
PRIOR PELING DATE: 2000-10-09
PRIOR PELING DATE: 2000-10-07
PRIOR PELING DATE: 2000-10-07
PRIOR PELING DATE: 2000-00-02
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                                                                                                                                                       Foy, Teresa M.
Watanabe, Yoshihiro
Meagher, Madeleine Joy
Yasir A. W.
William T.
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Best Local Similarity 64.5
Matches 160; Conservative
                                                       John
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ORGANISM: Homo sapiens
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                                                                                                                     APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
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Pred. No. 5e-19;
0; Mismatches 28; Indels
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PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR PLING DATE: 2005-03-14
                     Sequence 32477, Application US/11266748A Publication No. US20060134663A1 GENERAL INFORMATION:
APPLICANT: Harkin, Paul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/700,293 PRIOR FILING DATE: 2005-07-18 SEQ ID NOS: 483996 SOFTWARE: Patentin version 3.3
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Publication No. US20060269532A1
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APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Renger, Gary R.
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79.1%;
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Day, Craig H.
Vedvick, Thomas S
Carter, Darrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 23.29
Best Local Similarity 79.1<sup>3</sup>
Matches 106; Conservative
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US-11-344-932-67/c
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LENGTH: 5449
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US-11-266-748A-58517/c
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SEQ ID NO 58517
LENGTH: 15439
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            CHERKAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
ITILE OF INVENTION: METHODS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND
ITILE OF INVENTION: METHODS FOR THEIR USE
FILE REFERENCE: 21002-1.4287
CURRENT APPLICATION NUMBER: US/11/349,541
CURRENT PILING DATE: 1998-07-02-06
PRIOR FILING DATE: 1998-07-14
PRIOR FILING DATE: 1998-02-25
PRIOR PILING DATE: 1998-02-02-09
PRIOR FILING DATE: 1998-02-03
PRIOR FILING DATE: 1998-02-03
PRIOR FILING DATE: 1997-08-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      171 CACAATCGIGGCTAGACTICTTTTAAGCAAGTCCCCTTTTTTAAAAGGGGAACTCTCA 112
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| Publication No. US20060194265A1
| GENERAL INCRMATION:
| APPLICANT: Malandro, Marc S.
| TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER FILE REFERENCE: 20366-066001
| CURRENT APPLICATION NUMBER: US/10/669,920
| CURRENT APPLICATION NUMBER: US/10/669,920
| CURRENT APPLICATION NUMBER: US/004,113
| PRIOR APPLICATION NUMBER: US 10/004,113
| PRIOR FILING DATE: 2001-10-03
| PRIOR FILING DATE: 2001-11-08
| PRIOR FILING DATE: 2001-11-08
| PRIOR FILING DATE: 2001-11-30
| PRIOR FILING DATE: 2001-12-20
| PRIOR FILING DATE: 2001-12-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 84; DB 10;
Pred. No. 6.7e-18;
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64.5%;
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Best Local Similarity 64.5
Matches 160; Conservative
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; ORGANISM: Homo sapien
US-11-349-541-67
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19.5%; Score 75.2; DB 8; Length 154394; larity 82.7%; Pred. No. 1.6e-13; Conservative 0; Mismatches 18; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20.1%; Score 77.2; DB 6; Length 25694; 79.8%; Pred. No. 1.3e-14; ive 0; Mismatches 23; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Johnston, Patrick
APPLICANT: Johnston, Rarl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 10/322,281
PRIOR FILING DATE: 2002-12-17
PRIOR PILING DATE: 2002-12-17
NUMBER OF SEQ ID NOS: 1441
SOFTWARE: PSECSEQ for Windows Version 4.0
SEQ ID NO 46
LENGTH: 25694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR PILING DATE: 2004-11-03
PRIOR PLING DATE: 2004-11-03
PRIOR PELING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2005-01-14
PRIOR PILING DATE: 2005-07-18
PRIOR PILING DATE: 2005-07-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 58517, Application US/11266748A Publication No. US20060134663A1 GENERAL INFORMATION:
APPLICANT: Harkin, Paul
                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (1)...(25694)
OTHER INFORMATION: n = A,T,C or G
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Best Local Similarity 79.8'
Matches 91; Conservative
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US-11-266-748A-58517
                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: misc_feature
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Best Local Similarity
Matches 86; Conserv
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Search completed: December 31, 2006, 19:49:14 Job time : 139.37 secs

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LENGTH: 385
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243.6
243.6
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APPLICANT:
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2: FBMC_Celerra_SIDS3/ptodate2/2/pubpna/US08_PUBCOMB.seq:*
3: FBMC_Celerra_SIDS3/ptodate3/2/pubpna/US08_PUBCOMB.seq:*
4: FBMC_Celerra_SIDS3/ptodate3/2/pubpna/US09_PUBCOMB.seq:*
5: FBMC_Celerra_SIDS3/ptodate3/2/pubpna/US09_PUBCOMB.seq:*
6: FBMC_Celerra_SIDS3/ptodate3/2/pubpna/US10_PUBCOMB.seq:*
7: FBMC_Celerra_SIDS3/ptodate3/2/pubpna/US10_PUBCOMB.seq:*
8: FBMC_Celerra_SIDS3/ptodate3/2/pubpna/US10_PUBCOMB.seq:*
10: FBMC_Celerra_SIDS3/ptodate3/2/pubpna/US10_PUBCOMB.seq:*
11: FBMC_Celerra_SIDS3/ptodate3/2/pubpna/US10_PUBCOMB.seq:*
12: FBMC_Celerra_SIDS3/ptodate3/2/pubpna/US10_PUBCOMB.seq:*
13: FBMC_Celerra_SIDS3/ptodate3/2/pubpna/US10_PUBCOMB.seq:*
14: FBMC_Celerra_SIDS3/ptodate3/2/pubpna/US11B_PUBCOMB.seq:*
15: FBMC_Celerra_SIDS3/ptodate3/2/pubpna/US11B_PUBCOMB.seq:*
16: FBMC_Celerra_SIDS3/ptodate3/2/pubpna/US11B_PUBCOMB.seq:*
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Sequence 11258, A
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7716.790 Million cell updates/sec
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Sequence 67, 1
Sequence 67, 1
                                                                                                                                December 31, 2006, 12:22:01; Search time 613.045 Seconds
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-198-846-11258
US-11-234-786-701
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US-09-780-669-67
US-09-030-66-67
US-09-822-827-67
US-09-915-453-67
US-09-895-793-67
US-09-895-793-67
US-10-11-2896-67
US-10-1144-678A-67
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                                                                                                                                                                                                                                                                                                                                                                               18892170 seqs, 6143817638 residues
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                                                                                      - nucleic search, using sw model
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Maximum Match 100%
Listing first, 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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385
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Match Length
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Sequence 824, Appleagement 289560, Sequence 289560, Sequence 289561, Sequence 289562, Sequence 289562, Sequence 366451, Sequence 979860, Sequence 979861, Sequence 979861, Sequence 979861, Sequence 979862, Sequence 366453, Sequence 2587, Appleagemente 25887, 
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Sequence 26115, P
Sequence 27673, P
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Sequence 7
Sequence 7
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US-09-759-143-701
US-09-805-701
US-09-805-701
US-09-805-701
US-09-805-701
US-10-102-805-701
US-10-104-678A-701
US-10-104-678A-701
US-10-104-678A-701
US-10-108-804-6224
US-09-925-065A-289560
US-09-925-065A-289561
US-09-925-065A-289561
US-09-925-065A-289561
US-09-925-065A-289562
US-10-301-480-379869
US-10-301-480-379862
US-10-301-480-979861
US-10-301-480-979861
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US-10-198-846-11429
US-10-357-930-21826
US-10-357-930-2115
US-10-357-930-27673
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ALIGNMENTS

Gaps APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427023
CURRENT PILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934 ő 0; Indels Query Match
100.0%; Score 385; DB 3; L
Best Local Similarity 100.0%; Pred. No. 2.2e-126;
Matches 385; Conservative 0; Mismatches 0; FastSEQ for Windows Version 3.0 ; Sequence 67, Application US/09759143; Patent No. US20020022248A1; GENERAL INFORMATION: Xu, Jiangchun
Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick TYPE: DNA ORGANISM: Homo sapien Li, Samuel

1 ACTACACACACTCCACTTGCCCTTGTGAGACACTTTGTCCCAGCACTTTAGGAATGCTGA

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210121.428C3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAAL, DAVID 4.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 2101:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0%;
Matches 385; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: (SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 385 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
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EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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STRANDEDNESS:
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US-09-030-606-67
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                                                                                                                 CCCTTTTAAAAAAGGGGACTTGCTTAAAAAAGAAGTCTAGCCACGATGTGTAGAGCAGC
                                                                                                                                                                                                     181 IGICTGTGCTGGAGATTCACTTTTGAGAGAGTTCTCCTCTGAGAGCTGTTCTTTAGAGG
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GGTCGGACCAGCCACATCTCATGTGCAAGATTGCCCAGCAGACATCAGGTCTGAGAGTTC
                                                                                                                                   TGTGCTGTGCTGGAGATTCACTTTTGAGAGTTCTCCTCTGAGACCTGATCTTTAGAGG
                                                                                                                                                                                                                                                 CTGGGCAGTCTTGCACATGAGATGGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG
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APPLICANT: Skelky, Yasir A.W.
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Hepler, William
APPLICANT: Hural, John
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C24
CURRENT APPLICATION NUMBER: US/09/780,669
CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
SOFTWARE: FastSEQ for Windows Version 3.0
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Best Local Similarity 100.0%; Pred. No. 2.2e-126;
Matches 385; Conservative 0; Mismatches 0;
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Patent No. US20020051977A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
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Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
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Henderson, Robert A.
Kalos, Michael D.
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Vedvick, Thomas S.
Carter, Darrick
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ORGANISM: Homo sapien
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Sequence 67, Application US/09030606
| Patent No. US20020081580A1
| GENERAL INFORMATION:
| APPLICANT: Xu, Jiangchun |
| APPLICANT: Dillon, Davin C. |
| TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHODS IS TITLE OF SEQUENCES: 224
| CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: SEED and BERRY LLP |
| STREET: 6300 Columbia Center, 701 Fifth Avenue |
| CITY: Seattle |
| STATE: WA |
| COUNTRY: USA
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COMPUTER: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/030,606
FILING DATE: 25-FEB-1998
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Patent No. US20020090372A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND TITLE OF INVENTION: COMPOUNDS FOR THEIR USE
FILE REFERENCE: 210121.427C4
CURRENT APPLICATION NUMBER: US/09/115,453B
CURRENT APPLICATION NUMBER: US/09/115,453B
CURRENT FILING DATE: 1998-07-14
NUMBER OF SEQ ID NOS: 228
SOFTWARE: FastSEQ for Windows Version 3.0
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Publication No. US20020182596A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer Lynn
ITTLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF
TITLE OF INVENTION: PROSTATE CANCER AND METHODS FOR THEIR USE
FILE REPERENCE: 210121.428C6
CURRENT APPLICATION NUMBER: US/09/232,880
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Pred. No. 2.2e-126;
; Mismatches 0;
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ORGANISM: Homo sapien
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US-09-115-453-67
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US-09-232-880-67
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.534C1
CURRENT APPLICATION NUMBER: US/09/822,827
CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 982
SEQ ID NO 67
LENGTH: 385
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Patent No. US20020081680A1
GENERAL INFORMATION:
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ORGANISM: Homo sapien
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APPLICANT: Foy, Teresa
APPLICANT: Foy, Teresa
APPLICANT: ADDEC GATY R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C26
CURRENT APPLICATION NUMBER: US/09/895,814
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                                                                                                                                                                                          100.0%; Score 385; DB 3; Length 385; 100.0%; Pred. No. 2.2e-126;
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CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 67
LENGTH: 385
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McNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
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; Sequence 67, Application US/09895814
; Publication No. US20020193296A1
; GENERAL INFORMATION:
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Glang, Yugiu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
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Hepler, William T.
Henderson, Robert A.
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Vedvick, Thomas S.
Carter, Darrick
Li, Samuel X.
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US-09-895-793-67
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Best Local Similarity
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APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.534C2
                                                                                                                                                                                              100.0%; Score 385; DB 3; Length 385; 100.0%; Pred. No. 2.2e-126; ive 0; Mismatches 0; Indels (
    CURRENT FILING DATE: 1999-01-15
NUMBER OF SEQ ID NOS: 338
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 67
LENGTH: 385
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Hural, John
McNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
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Publication No. US20020192763A1
GENERAL INFORMATION:
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APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Rolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Vedvick, Thomas S.
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Skeiky, Yasir A.W.
Hepler, William T.
                                                                                                                                                                                              Query Match 100.
Best Local Similarity 100.
Matches 385; Conservative
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                                                                                                                 TYPE: DNA
ORGANISM: Homo sapien
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US-09-895-793-67
                                                                                                                                                        US-09-232-880-67
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61 GGTCGGACCAGCCACATCTCATGTGCAAGATTGCCCAGCAGACATCAGGTCTGAGAGTTC 120
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                                                                                                                                                                                                                                                   Length 385;
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APPLICANT: Fanger, Gary
APPLICANT: Retter, Mark
APPLICANT: Solk, John
APPLICANT: Solk, John
APPLICANT: Only Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                100.0%; Score 385; DB 6; L
100.0%; Pred. No. 2.2e-126;
tive 0; Mismatches 0;
                   CURRENT APPLICATION NUMBER: US/10/012,896
UNERBY FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: PASTSEQ for Windows Version 3.0
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SOCTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 67
LENGTH: 385
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CURRENT APPLICATION NUMBER: US/10/010,940
CURRENT FILING DATE: 2001-12-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361 CATAGTTTCTGTGCTAGTGGACCGT 385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitchem, Jennifer L.
APPLICANT: Harlocker, Susan Louise
FILE REFERENCE: 210121.427C27
                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 385; Conservative
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Reed, Steven G.
                                                                                                                                                                                ORGANISM: Homo sapiens
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; ORGANISM: Homo sapien
US-10-010-940-67
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US-10-010-940-67
                                                                                                             SEQ ID NO 67
LENGTH: 385
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APPLICANT: Wantanabe, Yoshihiro
APPLICANT: Meagher, Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
                                                                                                                                                                                                        Length 385;
                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                     100.0%; Score 385; DB 3; L
ilarity 100.0%; Pred. No. 2.2e-126;
Conservative 0; Mismatches 0;
                   NUMBER OF SEQ ID NOS: 990
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 67
LENGTH: 385
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McNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
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Publication No. US20020183251A1
GENERAL INPORMATION:
APPLICANT: Witcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: ARlos, Michael D.
APPLICANT: Stolk, John A.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Carter, Marc M.
APPLICANT: Carter, Marc M.
APPLICANT: Li, Samiel X.
2001-06-29
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Hepler, William T.
Henderson, Robert A.
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                                                                                                 TYPE: DNA
) ORGANISM: Homo sapien
US-09-895-814-67
CURRENT FILING DATE:
                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 385; Conserv
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US-10-012-896-67
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us-09-232-880-67.rnpbm

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100.0%; Pred. No. 2.2e-126;
ive 0; Mismatches 0;
                               100.0%; Score 385; DB 7; I 100.0%; Pred. No. 2.2e-126;
                                                                   0; Mismatches
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                                                                     Matches 385; Conservative
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US-10-294-025-67
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US-10-144-678A-67
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                                 Gaps
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121-427C28
CURRENT APPLICATION NUMBER: US/10/144,678A
CURRENT FILING DATE: 2002-08-12
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Length 385;
                                   Indels
100.0%; Score 385; DB 6; L
100.0%; Pred. No. 2.2e-126;
ive 0; Mismatches 0;
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Skeiky, Yaair A. W.
Hepler, William T.
Hural, John
McNeill, Patricia D.
Houghton, Raymond L.
Vinals y de Bassols, Carlota
Foy, Teresa M.
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 67
LENGTH: 385
TYPE: DNA
ORGANISM: Homo sapiens
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US-10-144-678A-67
IS-10-144-678A-67
Sublication US/10144678A
GENERAL INFORMATION:
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Ralos, Michael D.
APPLICANT: Rater, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
Query Match 100.
Best Local Similarity 100.
Matches 385; Conservative
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                                                                                                                                                                                                                                                                                                                      Sequence 67, Application. US/10688838

Publication No. US20040141989A1

GENERAL INFORMATION:

APPLICANT: Vu, Jiangchun

TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE

TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE

FILE REFERENCE: 21011.42794

CURRENT APPLICATION NUMBER: US/10/688,838

CURRENT FILING DATE: 2003-10-17

NUMBER OF SEQ ID NOS: 228

SOFTWARE: PSELSEQ for Windows Version 4.0

SEQ ID NO 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 385; DB 8; Length 385; 100.0%; Pred. No. 2.2e-126; ive 0; Mismatches 0; Indels
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US-11-234-786-67
Sequence 67, Application US/11234786
Publication No. US20060024301A1
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Matches 385; Conservative
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CORGANISM: Homo sapiens
US-10-688-838-67
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US-10-688-838-67
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APPLICANT: SAEIK, Yasair A.
TITLE OF INVENTION: PROSTATE-SPECIFIC POLYPEPTIDES AND FUSION
TITLE OF INVENTION: POLYPEPTIDES THEREOF
FILE REPERENCE: 210121.427C31
CURRENT PILING DATE: 2005-09-23
FRICH APPLICATION NUMBER: US 09/568,857
PRIOR PILING DATE: 2000-05-09
PRIOR FILING DATE: 2000-06-07
PRIOR FILING DATE: 2000-06-07
PRIOR PLING DATE: 2000-06-01-14
PRIOR FILING DATE: 2000-06-01-14
PRIOR FILING DATE: 2000-01-14
PRIOR PLING DATE: 2000-01-14
PRIOR PLING DATE: 2000-01-14
PRIOR PLING DATE: 2000-01-14
PRIOR PLING DATE: 1999-11-12
PRIOR PLING DATE: 1999-11-12
PRIOR PLING DATE: 1999-11-13
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PRIOR APPLICATION NUMBER: US 09/150,607
PRIOR APPLICATION NUMBER: US 09/030,607
PRIOR APPLICATION NUMBER: US 09/030,607
PRIOR PLING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: US 09/030,607
PRIOR PLING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: US 09/030,607
PRIOR PLING DATE: 1998-02-25
PRIOR PLING DATE: 1998-07-14
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Xu, Jiangchun
Dillon, Davin C.
Mitchan, Jennifer L.
Harlocker, Susan L.
Jiang, Yugiu
Reed, Steven G.
Ralos, Michael D.
Fanger, Gary R.
Fetter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
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241 CTGGGCAGTCTTGCACATGAGATGGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG 300
                                                             301 CCTCTCCCAGGGCCCCAGCCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCCATAC 360
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US-10-294-025-1036
US-10-294-025-1036
Sequence 1036, Application US/10294025
Publication No. US20030185830A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun A.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C29
CURRENT APPLICATION NUMBER: US/10/294,025
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 1038
SOUTHWARE: FEBELSEQ for Windows Version 3.0
SEQ ID NO 1036
LENGTH: 3710
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CORGANISM: Homo sapiens
US-10-294-025-1036
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; Search time 89.8616 Seconds (without alignments) 8016.516 Million cell updates/sec
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| FBMC_Celerra_SIDS3/ptodata/2/ina/6_COMB.seq:*
| FBMC_Celerra_SIDS3/ptodata/2/ina/6_COMB.seq:*
| FBMC_Celerra_SIDS3/ptodata/2/ina/6_COMB.seq:*
| FBMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
| FBMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
| FBMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
| FBMC_Celerra_SIDS3/ptodata/2/ina/PCTUMB.seq:*
| FBMC_Celerra_SIDS3/ptodata/2/ina/PCTUMB.seq:*
| FBMC_Celerra_SIDS3/ptodata/2/ina/PCTUMB.seq:*
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Sequence 701,
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Sequence 7
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-09-679-426-701
US-09-759-143-701
US-09-651-236-701
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US-09-030-607-67
US-09-439-313-67
US-09-232-149A-67
US-09-159-812-67
US-09-685-166A-67
US-09-685-166A-67
US-09-685-166A-67
US-09-679-426-67
US-09-679-426-67
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US-09-651-236-67
US-09-651-236-67
US-09-651-236-67
US-09-651-236-67
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US-09-651-236-67
US-09-651-236-67
US-09-67-279-67
US-09-116-114-67
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                                                                                                                                        December 31, 2006, 12:18:37
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                                                                                            OM.nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                             IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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385
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No.
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Gaps

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Length 385;

Query Match
100.0%; Score 385; DB 3; Length 30
Best Local Similarity 100.0%; Pred. No. 5.9e-124;
Matches 385; Conservative 0; Mismatches 0; Indels

ORGANISM: Homo sapiens US-09-020-956-67

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     Length 385
                                         Indels
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APPLICANT Harlocker, Susan Louise
APPLICANT Harlocker, Susan Louise
APPLICANT Gred, Steven G.
APPLICANT Seed, Steven G.
APPLICANT Reed, Steven G.
APPLICANT Reds, Michael
APPLICANT Retter, Mark
APPLICANT Solk, John
APPLICANT BOLK, John
APPLICANT DIAGNOSITIONS AND METHODS FOR THEF
ITTLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
ITTLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
ITTLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
ITTLE OF INVENTION: 1999-11-12
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 67
LENGTH: 385
; Score 385; DB 3; 1; Pred. No. 5.9e-124; 0; Mismatches 0;
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
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     100.0%;
100.0%;
     Query Match
Best Local Similarity 100.
Matches 385; Conservative
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CORGANISM: Homo sapien
US-09-439-313-67
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Best Local Similarity
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US-09-439-313-67
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Patent No. 6262245
GENERAL INFORMATION:
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS INTERESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/030,607
FILING DATE: 25-FEB-1998
CLASSIFICATION:
NAME: Maki, David J.
REGISTRATION:
REPERBENCE/DOCKET NUMBER: 31,392
REPERBENCE/DOCKET NUMBER: 210121.427C3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
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TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNES: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
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CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104
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US-09-030-607-67
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Patent No. 6613872
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
TTITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF
TITLE OF INVENTION: PROSTATE CANCER AND METHODS FOR THEIR USE
TITLE OF INVENTION NUMBER: US/09/159,812A
CURRENT APPLICATION NUMBER: US/09/159,812A
CURRENT PILICATION NUMBER: US/09/159,812A
NUMBER OF SEQ ID NOS: 306
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 385;
                                                                                                                                                                                                                APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Micham, Jevin C.
APPLICANT: Micham, Jennifer Lynn
TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
TITLE OF ILINGDIAL 2706
CURRENT APPLICATION NUMBER: US/09/232,149A
CURRENT APPLICATION NUMBER: US/09/232,149A
SOFTWARE: FREE OF WINDOWS 338
SOFTWARE: FREE OF WINDOWS Version 3.0
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100.0%; Score 385; DB 3; Length 3
Best Local Similarity 100.0%; Pred. No. 5.9e-124;
Matches 385; Conservative 0; Mismatches 0; Indels
                            361 CATAGTTTCTGTGCTAGTGGACCGT 385
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361 CATAGITICIGIGCIAGIGGACCGI 385
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US-09-322-149A-67
Sequence 67, Application US/09232149A
; Patent No. 6465611
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US-09-159-812-67
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LENGTH: 385
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Patent No. 6395278

Geguence 67, Application US/09352616A

Patent No. 6395278

GENERAL INFORMATION:

APPLICANT: Dilang, Yuqui

APPLICANT: Jiang, Yuqui

APPLICANT: Xu, Jiangchun

APPLICANT: Xu, Jiangchun

TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS

TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE

FILE REFERENCE: 210121.427C8

CURRENT FILING DATE: 1999-07-13

NUMBER OF SEQ ID NOS: 472

SEQ ID NO 67

ENGTHARE: PastSEQ for Windows Version 3.0

SEQ ID NO 67

ENGTHARE: ABS
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Best Local Similarity 100.
Matches 385; Conservative
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ORGANISM: Homo sapien
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Sequence 67, Application US/09685166A, Patent No. 6630305
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
          Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 385; Conservative 0;
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Best Local Similarity 100.
Matches 385; Conservative
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ORGANISM: Homo sapien
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APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Wasix A.W.
APPLICANT: Wasix A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: COMPOSITIONS OF PROSTATE CANCER
FILE REFERENCE: 21011.42717C17
CURRENT APPLICATION NUMBER: US/09/636,215
CURRENT FILING DATE: 2000-08-10
NUMBER OF SECIENOS: 852
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                                                                                          100.0%; Score 385; DB 3; Length 385; 100.0%; Pred. No. 5.9e-124; Live 0; Mismatches 0; Indels
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Patent No. 6620922
GENERAL INFORMATION:
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Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
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Dillon, Davin C.
Mitcham, Jennifer L.
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                                                                                             Query Match 100.
Best Local Similarity 100.
Matches 385; Conservative
                         TYPE: DNA
, ORGANISM: Homo sapien
US-09-159-812-67
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CRGANISM: Homo sapien
US-09-636-215-67
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LENGTH: 385
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                 LENGTH: 385
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APPLICANT: Jiang, Yuqui
APPLICANT: Jiang, Yuqui
APPLICANT: Henderson, Robert A.
APPLICANT: Ralos, Michael D.
APPLICANT: Ralos, Michael D.
APPLICANT: Retter Marc W.
APPLICANT: Retter, Dan A.
APPLICANT: Day, Craig H.
APPLICANT: Day, Craig H.
APPLICANT: Wang, Thomas S.
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE
CURRENT FILING DATE: 2000-10-10
CURRENT APPLICATION NUMBER: US/09/685,166A
CURRENT FILING DATE: 2000-10-10
NUMBER OF SEQ ID NOS: 898
SOFTWARE: FASTESQ for Windows Version 3.0
SEQ ID NO 67
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Score 385; DB 3; Length 385;
Pred. No. 5.9e-124;
                                                   0; Indels
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                                                                                                                                                                                                   Sequence 67, Application US/09688489;
Sequence 67, Application US/09688489;
Fatent No. 6664377;
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun;
APPLICANT: Mitcham, Jennifer Lynn;
TITLE OF INVENTION: COMPOUNDE FOR IMMUNOTHERAPY OF PROSTATE;
TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE;
FILE REFERENCE: 210121.42702;
CURRENT APPLICATION NUMBER: US/09/688,489;
CURRENT APPLICATION NUMBER: US/09/688,489;
CURRENT APPLICATION NUMBER: US/09/688,489;
NUMBER OF SEQ ID NOS: 338;
SOFTWARE: FRASESQ for Windows Version 3.0
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Patent No. 6755515
GRUBRAL INFORMATION:
APPLICANT: Xu, Janagchun
APPLICANT: Dillon, Davin C.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jinng, Yuqui
                                                                          361 CATAGTTTCTGTGCTAGTGGACCGT
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US-09-688-489-67
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SEQ ID NO 67
LENGTH: 385
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US-09-679-426-67
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Patent No. 6657056
GENERAL INFORMATION:
APPLICANT: VI. Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND TITLE OF INVENTION: WHETHOOS FOR THEIR USE FILE REPERENCE: 210121.427C4
CURRENT APPLICATION NUMBER: US/09/115,453B
CURRENT APPLICATION NUMBER: US/09/115,23B
NUMBER OF SEQ ID NOS: 228
SOFTWARE: FastSEQ for Windows Version 3.0
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Best Local Similarity 100.0%; Pred. No. 5.9e-124;
Matches 385; Conservative 0; Mismatches 0;
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US-09-115-453-67
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US-09-115-453-67
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                                                              APPLICANT: L1, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121-427C23
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSEQ for Windows Version 3.0
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Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
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Vedvick, Thomas S.
Carter, Darrick
Li, Samuel
Wang, Aijun
      Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
Li, Samuel
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Best Local Similarity 100.
Matches 385; Conservative
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CORGANISM: Homo sapien
US-09-759-143-67
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APPLICANT:
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APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Ranger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Bedvick, John A.
APPLICANT: Day, Craig H.
APPLICANT: Uedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Wang, Aljun
APPLICANT: Hepler, William
APPLICANT: Hepler, William
APPLICANT: Hepler, William
APPLICANT: Hepler, William
APPLICANT: Hepler, William
APPLICANT: Hepler, William
APPLICANT: Hepler, William
APPLICANT: Skeiky, Yasers, Vowenstrone Composition of PROSTATE CANCER
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427220
CURRENT APPLICATION NUMBER: US/09/679,426
CURRENT FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 895
SOFURM SEQ ID NOS: 895
SSEQ ID NO 67
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US-09-759-143-67
Sequence 67, Application US/09759143
Patent No. 6800746
GENERAL INFORMATION:
APPLICANT: W. Jiangchun
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
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Best Local Similarity 100.0
Matches 385; Conservative
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ORGANISM: Homo sapien
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                                                                  210121.428C3
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                                                                                 TELECOMMUNICATION INFORMATION:
TELEPAN: (206) 622-4900
TELEPAN: (206) 622-4900
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 385 Base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
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Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
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ATTORNEY/AGENT INFORMATION:
                      NAME: Maki, David J.
REGISTRATION NUMBER: 31,
REFERENCE/DOCKET NUMBER:
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Vedvick, Thomas S
Carter, Darrick
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Dillon, Davin C.
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Hepler, William
                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Homo sapiens
US-09-030-606-67
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Sequence 67, Application US/09030606
Sequence 67, Application US/09030606
Sequence 67, Application US/09030606
GENERAL INFORMATION:
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHODS INFORMER OF SEQUENCES: 224
CORRESPONDENCE ADDRESS: 224
COMPRESPONDENCE ADDRESS: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
STREET: WA
COUNTRY: USA
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       APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.42718C18
CURRENT APPLICATION NUMBER: US/09/651,236
CURRENT FILING DATE: 2000-08-29
NUMBER OF SEQ ID NOS: 865
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 385
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                                                                                                                                                                                                                                                                                                                                                         Length 385;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/030,606
FILING DATE: 25-FEB-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 385; DB 3; L
Best Local Similarity 100.0%; Pred. No. 5.9e-124;
Matches 385; Conservative 0; Mismatches 0;
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Skeiky, Yasir A.W.
                                                                                                                                                                                                                                                         TYPE: DNA
CORGANISM: Homo sapien
US-09-651-236-67
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; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND FITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER; FILE REPERBENCE: 210121.427C19
; CURRENT APPLICATION NUMBER: US/09/657,279
; CURRENT APPLICATION NUMBER: 2000-09-06
; NUMBER OF SEQ ID NOS: 877
; SEQ ID NO 67
; LENGTH: 385
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-657-279-67
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Search completed: December 31, 2006, 12:31:10 Job time : 90.8616 secs

Acrosolo Breast ca Acf6684 Human pro Aab93865 P704P cDN Aas64037 Human pro Aca59845 Prostate Acc95572 Prostate Adb14151 Human pro Add26567 Human pro Add26567 Human pro Add2664 Human bre Aal12944 Human bre Aal18894 Human bre

Acn87074 Breast ca Acn84137 Breast ca Abv26126 Human pro Abv27659 Human pro Abv21835 Human pro

Sequence:

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Searched:

Database

Result No.

Acn90279 Breast ca Aal14082 Human bre Acn81332 Breast ca Aal15514 Human bre Aal24358 Human bre Acn85503 Breast ca Acn91316 Breast ca

al11453 Human bre Acn81654 Breast ca Aal18756 Human bre Aal20352 Human bre Aal11453 Human bre

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Novel human prostate specific tumour protein and fragments - useful detecting and treating prostate cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prostate tumour specific gene; human; prostate cancer; detection;
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ACN84137
ABV26126
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ACN90279
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ACN85503
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97US-00904809.
98US-00020747.
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08-DEC-1998
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              GenCore version 5.1.9 (c) 1993 - 2006 Biocceleration Ltd.
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This sequence represents a human prostate tumour specific gene, and can be used in the method of the invention. The method is for detecting prostate cancer comprises contacting a biological sample with an agent able to bind an immunogenic portion of a prostate protein (such as

for

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385
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98US-00159812.
99US-00159822.
99US-00232149.
99US-00232880.
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Best Local Similarity 100.0%;
Matches 385; Conservative 0
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23-SEP-1998;
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15-JAN-1999;
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encoded by this sequence). An antibody which binds to an immunogenic portion of the prostate protein, and the method can be used to detect, amintor progression of, or treat prostate cancers. The antibody may also be conjugated to a therapeutic agent for use in therapy of prostate cancers. (Updated on 25-MAR-2003 to correct PR field.)
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                                                           Sequence 385 BP; 86 A; 105 C; 94 G; 100 T; 0 U; 0 Other;
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The present sequence is a DNA which encodes an immunogenic portion of a prostate tumour protein. The encoded immunogen, or the DNA itself, can be used as a vaccine for the treatment of prostate cancer. The DNA was identified by analysis of a subtracted cDNA library obtained by subtracting a prostate tumour cDNA expression library with a normal tissue cDNA library
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US2002090372-A1
           Homo sapiens.
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                                                                                                                                             The present invention describes isolated polypeptides, comprising an immunogenic portion of a prostate tumour protein (PTP). The polypeptides and polymucleotides encoding them have cytostatic activity and can be used in vaccines encoding them have cytostatic activity and can be polypeptides and in gene therapy. The polypeptides and polypeptides are polypeptides and polypeptides and polypeptides and vaccines comprising them can be used for inhibiting the development of prostate cancer in a patient. The polypeptides can be used to generate antibodies or antibodies for passive immuno therapy. A portion of the polymucleotides encoding the polypeptides can be used as a probe or to modulate the expression of the polypeptides. AAA06241 to AAA06691 and AAX82000 to AAX82000 represent sequences used in the exemplification of
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prostate cancer; cytostatic; vaccine; 88.
                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 385; DB 3; Length 385; 100.0%; Pred. No. 1.8e-117; ive 0; Mismatches 0; Indels 0
                                                                                   New polypeptide useful for treating and diagnosing prostate comprises an immunogenic portion of prostate tumor protein.
                                                                                                                                                                                                                                                                                                                                  Sequence 385 BP; 86 A; 105 C; 94 G; 100 T; 0 U; 0 Other;
                                     Mitcham JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human prostate tumour protein partial DNA sequence #67
                                     Χu J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATAGTTTCTGTGCTAGTGGACCGT 385
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                                   Yuqiu J,
                                                                                                                        Claim 50; Page 120; 263pp; English.
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Best Local Similarity 100.0%;
Matches 385; Conservative 0
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                                   SF,
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                                                                                                                                                                                                                                                                                                         the present invention
          (CORI-) CORIXA CORP.
                                                           WPI; 2000-171268/15
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The present invention relates to a new polypeptide comprising an immunogenic portion of a prostate protein. The invention is useful for inhibiting the development of prostate cancer in a patient. The invention is also useful as markers for diagnosing prostate cancer and for monitoring diseases progression in patients. The present nucleic acid sequence represents a DNA sequence that is part of a gene encoding a human prostate tumour protein
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69 (119,453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 385; DB 3; L
100.0%; Pred. No. 1.8e-117;
iive 0; Mismatches 0;
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97US-00904804.
98US-00020956.
98US-00030607.
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(DILL/) DILLON D C.
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CCTCTCCCAGGGCCCCAGCCTGGCAACCTGCTTACAGGGCACTCCTCAGATGCCCATAC 360
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Matches 385; Conservative
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06-SEP-2000;
02-OCT-2000;
10-OCT-2000;
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09-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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12-MAY-2000;
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                                                                                                                                                                                                                                                                29-JAN-2002
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Li SX,
                                                                                                                                                                                                                                                                                                                                  Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Χu J,
                                                                                                                                                                 RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes polynucleotide sequences (I) which encode prostate-specific proteins (II). (I) and (II) have cytostatic activity, and can be used in vaccine production and gene therapy. (I), (II), antibodies to (II), fusion proteins comprising (II), and isolated I prepared using (I) or (II) are used treat cancer in a patient. (I) and the antibodies are also used in the detection of cancer in a patient. The cancer that is disgnosed or treated is particularly prostate cancer. (I) and (II) can be used in vaccines. The antibodies or (I) can be used for monitoring the progression of cancer in a patient. (I) and (II) can be used to improve disgnostic and therapeutic methods for prostate cancer. They can indicate the level of metastasis as well as the prostate volume. AAH933357 to AAH93944 and AAM01115 to AAM01318 represent
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for use in
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                                                                                                                                                                                                                                                                                                                                                  Harlocker SL, Jiang Y, Reed SG;
Retter MW, Stolk JA, Skeiky YAW;
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0
                                                                                            Human; prostate cancer; prostate-specific; diagnosis; vaccine; cytostatic; gene therapy; metastasis; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polynucleotide encoding a prostate-specific protein, monitoring and treating prostate cancer in a patient and
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                                                                Human prostate-specific cDNA sequence P80 (also P740P).
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Best Local Similarity 100.0%; Pred. No. 1.8e-117;
Matches 385; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 250; 543pp; English
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Kalos MD, Fanger GR, Day CH,
Wang A, Meagher MJ;
                                                                                                                                                                                                                                                   16-JAN-2001; 2001WO-US001574.
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                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-425873/45.
                                                                                                                                                                                  WO200151633-A2
                                                                                                                                                   Homo sapiens.
                                04-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vaccines.
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AAH93423;
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301 CCTCTCCCAGGGCCCCAGCCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCCATAC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New human prostate-specific polypeptides and polynucleotides useful for the diagnosis and treatment of cancer, especially prostate cancer.
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Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prostate cancer; ss; cytostatic; immunostimulant; tumour.
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A, Day CH, Vedvick TS,
spler WT, Henderson RA;
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                                                                                                                                                                  CATAGITICIGIGCTAGIGGACCGI 385
                                                                                                    CATAGTTTCTGTGCTAGTGGACCGT
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                                                                                                                                                                                                                                                                                                                                     BP.
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2000US-00570737.
2000US-00507737.
2000US-00605783.
2000US-00635125.
2000US-00657279.
2000US-006797279.
2000US-00679426.
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Mitcham JL, H
MW, Stolk JA,
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99US-00443686
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                                                                                                                                                                                                                                                                                                                                                                                                       요
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                                                                 GGTCGGACCAGCCACATCTCATGTGCAAGATTGCCCAGCAGACATCAGGTCTGAGAGTTC
                    CCCTTTTAAAAAAGGGGGACTTGCTTAAAAAAGAAGTCTAGCCACGATTGTGTAGAGCAGC
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prostate cancer;
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presence or absence of a cancer or monitoring the progression progression of a cancer, especially prostate cancer. AAH02422 AAB14798 to AAB14821 and AAB14830 are sequences used in the exemplification of the present invention
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                                                                                                                                                                                                     Length 385;
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, Day CH, Skeiky YAW,
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                                                      The present invention describes an isolated polypeptide (PI) comprising at least an immunogenic portion of a prostate-specific protein, or its variant. Also described are polymcleotides (NI) encoding (PI). (PI) and (NI) have cytostatic activity and can be used in vaccine production. The polypeptides, nucleic acids and antibodies from the present invention are useful in the diagnosis and therapy of prostate cancer. Prostate specific genes P704P, P712P, P77PB and B305D are located in a genomic region on chromosome 22q11.2 known as the Cat Eye Syndrome region.

AAH84671 to AAH85143 and AA9990000 to AAG99077 represent polynucleotide and polypeptide sequences used in the exemplification of the present
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chromosome 11p13; zinc finger transcription factor; 89.
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prostate-specific protein, useful in the diagnosis and therapy prostate cancer.
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                                       31; Page 150; 325pp; English
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                                                                                                                                                                                                                                                                                                                                                           The present invention describes compositions comprising peptides derived from the Wilm's tumour protein WT1 and methods for their use in treating mailgrant diseases. Peptides derived from both the murine and human WT1 proteins are provided. The human WT1 gene is found on chromosome 11p13, and the protein was shown to be a zinc finger transcription factor. The immunogenic peptides of the invention are particularly useful in the diagnosis and treatment of cancer and leukaemia. The present sequence is a coding sequence used in the exemplification of the invention
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                                                                                                                                                                                                 Polypeptide comprising part of the Wilms Tumor gene product sequence is used in the diagnosis and treatment of malignant diseases e.g. leukemia and cancer associated with WII.
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                                                                                                                                                                                                                                                                                                               Disclosure; Page 213-214; 228pp; English.
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99US-0157459P
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Best Local Similarity 100.
Matches 385; Conservative
                                                                                                                                                          WPI; 2001-328324/34
                                              (CORI-) CORIXA CORP
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GGTOGGACCAGCACACATCTCATGTGCAAGATTGCCCAGCAGACATCAGGTCTGAGAGTTC 120
                                                                                                                                                                           CCTCTCCCAGGGCCCCAGGCCAGGCCACCTGCTTACAGGGCACTCTCAGATGCCCATAC 360
                                                                                                                                                                                                301 CCTCTCCCAGGGCCCCAGCCTGGCTACAGGGCACTCTCAGATGCCCATAC 360
                                                                                                                                         CTGGGCAGTCTTGCACATGAGATGGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG
                                                 181 TGTGCTGTGCTGGAGATTCACTTTTGAGAGAGTTCTCCTCTGAGACCTGATCTTTAGAGG
                                                                                             CTGGGCAGTCTTGCACATGAGATGGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG
                                   CCCTTTTAAAAAAGGGGACTTGCTTAAAAAAGAAGTCTAGCCACGATTGTGTAGAGCAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prostate specific protein and its encoding polynucleotide, useful for the
                                                                                                                                                                                                                                                                                                                                                                                                                        Kalos MD;
Carter D;
Hural J;
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Pred. No. 1.8e-117;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         segdata.uspto.gov/seguence.html?DocID=US20020192763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   treatment and diagnosis of prostate cancer
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100.0%;
                                                                               29-JUN-2001; 2001US-00895793.
                                                                                                     04-OCT-1999; 99US-0157455P.
04-OCT-2000; 2000US-00679272.
28-MAR-2001; 2001US-00822827.
                                                                                                                                                                                                                                                                                                                                                                                                                       Ku J, Fanger GR, Ker. Sanger GR, Wang A, Skela, SK, Wang A, Skela, Houghton RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               format directly from the US
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Matches 385; Conservative
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WANG A.
SKEIKY Y A W.
HEPLER W T.
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Y DE BASSOLS C
FOY T M.
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MITCHAM J L.
HARLOCKER S I
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DAY C H.
VEDVICK T S.
CARTER D.
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MCNEILL P D.
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RETTER M W.
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                                                                                                                                                                                                  JIANG Y.
                                    US2002192763-A1
              Homo sapiens.
                                                          19-DEC-2002
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(FOYT/)
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(KALO/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel polynucleotide encoding polypeptide comprising a portion of prostate tumor protein useful for inhibiting development of prostate cancer or for treating prostate cancer in a patient.
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100.0%; Score 385; DB 5; L
Best Local Similarity 100.0%; Pred. No. 1.8e-117;
Matches 385; Conservative 0; Mismatches 0;
CATAGITICIGIGCIAGIGGACCGI 385
                                                     361 CATAGITITCIGIGCTAGIGGACCGT 385
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                                                                                                                                                                                                  AAS10066 standard; cDNA; 385 BP
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97US-00904804.
98US-00020956.
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            JIANG Y.
KALOS M D.
FANGER G R.
RETTER M W.
STOLK J A.
DAY C H.
VEDVICK T S.
CARTER D.
LI S X.
WANG A.
REPLER W T.
HEDLERW Y A W.
HARLOCKER S
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Fanger G
Li SX,
            (JIAN/)
(KALO/)
(FANG/)
(RETT/)
(STOL/)
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                 GGTCGGACCAGCCACATCTCATGTGCAAGATTGCCCAGCAGACATCAGGTCTGAGAGTTC
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01-AUG-1997; 97US-00904804.
15-FEB-1998; 98US-00020956.
25-FEB-1998; 98US-00130607.
14-UUL-1998; 98US-00159812.
15-JAN-1999; 99US-00159812.
12-NOV-1999; 99US-0028246.
13-JUL-1999; 99US-00282616.
12-NOV-1999; 99US-0044366.
14-JAN-2000; 2000US-0044366.
14-JAN-2000; 2000US-0059817.
09-MAY-2000; 2000US-0058193.
13-JUN-2000; 2000US-0058193.
13-JUN-2000; 2000US-0058173.
13-JUN-2000; 2000US-0058173.
13-JUN-2000; 2000US-0058173.
13-JUN-2000; 2000US-0058173.
13-JUN-2000; 2000US-0058173.
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10-OCT-2000; 2000US-00685166.
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DILLON D C.
MITCHAM J L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention provides prostate-specific coding sequences and their encoded proteins. These can be used in the diagnosis and treatment of cancers, particularly prostate cancer. The present sequence is a CDNA described in the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 GGTCGGACCACACATCTCATGTGCAAGATTGCCCAGCAGACATCAGGTCTGAGAGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGGGCAGTCTTGCACATGAGATGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
  Ď.;
                                                                                                                                             New prostate-specific polynucleotides for diagnosing and treating diseases, in particular prostate cancer, and as markers for the progression of cancer.
  Kalos M
Carter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 385; DB 6; Length 385; Best Local Similarity 100.0%; Pred. No. 1.8e-117; Matches 385; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 385 BP; 86 A; 105 C; 94 G; 100 T; 0 U; 0 Other;
Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATAGITICTGTGCTAGTGGACCGT 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATAGITICIGIGCIAGIGGACCGI 385
                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 67; 87pp; English.
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The present invention relates to novel prostate-specific proteins (PSP) and their coding sequences. The PSPs and their coding sequences are useful for stimulating an immune response in a patient, or for treating prostate cancer in a patient and for determining, detecting or diagnosing the presence of a cancer in a patient. The present sequence was used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New prostate-specific proteins and genes, useful in gene therapy, particularly for stimulating an immune response in a patient, or treating prostate cancer in a patient, as well as for diagnosing prostate cancer
 301 CCTCTCCCAGGGCCCCAGCCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCCATAC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jiang Y, Henuca
Day CH, Vedvick TS;
ler WT, Hural J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGTCGGACCAGCCACATCTCATGTGCAAGATTGCCCAGCAGACATCAGGTCTGAGAGTTC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ACTACACACACTCCACTTGCCCTTGTGAGACACTTTGTCCCAGCACTTTAGGAATGCTGA
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                                                                                                                                                                                                                                                                                                                          prostate-specific protein; PSP; human; cancer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lon DC, Mitcham JL, Harlocker SL, Jiang Y, H. Fanger GR, Retter MW, Stolk JA, Day CH, Ved-Li SX, Wang A, Skeiky YAW, Hepler WT, Hural Houghton RL, Vinals Y De Bassolsc, Foy TM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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Best Local Similarity 100.0%; Pred. No. 1.8e-117;
Matches 385; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                     Prostate tumour specific cDNA sequence SEQ ID 67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 3; Page 317; 691pp; English.
                                       CATAGTTTCTGTGCTAGTGGACCGT
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29-JUN-2001; 2001US-00895814.
10-DEC-2001; 2001US-00012896.
                                                                                                                                                                      ACC95051 standard; cDNA; 385
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                                                                                                                                                                                                                                                                                                                          therapy;
prostate
                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                response;
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Carter D, Li
Mcneill PD,
                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                                                                                                                                                                 28-AUG-2003
                                                                                                                                                                                                                                                                                                                          Cytostatic;
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                                     361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a method of detecting prostate cancer by contacting a biological sample from a patient with: (a) a binding agent that binds to a polypeptide having an immunogenic portion of a prostate protein or its variant; (b) 2 oligonucleotide primers, where 1 of the oligonucleotides is specific for a DNA encoding the polypeptide of (a); or (c) an oligonucleotide probe specific for a DNA molecule encoding the polypeptide of (a). The method and polypeptides are useful for diagnosing, treating, particularly by immunotherapy, monitoring the progression, and inhibiting the development of prostate cancer in a patient. The polypeptides may be used to generate antibodies useful for the diagnosis and monitoring of prostate cancer. ABSSB350-ABSSB346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGGGCAGTCTTGCACATGAGATGGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Detecting prostate cancer comprises contacting a sample with an agent capable of binding to a polypeptide with an immunogenic portion of a prostate protein, oligonucleotide primers or a probe specific for DNA encoding the polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACTACACACACTCCCACTTGCCCTTGTGAGACACTTTGTCCCCAGCACTTTAGGAATGCTGA
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                                                                         tumour; immunotherapy; prostate cancer; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Length 385;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 385; DB 6; L
Pred. No. 1.8e-117;
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97US-00904809.
98US-00020747.
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(first entry)
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Matches 385; Conservative
                                     tumour cDNA
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DILLON D C.
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09-FEB-1998;
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05-NOV-2002
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                                     Prostate
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                                                      CTGGGCAGTCTTGCACATGAGATGGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG 300
                                                                                                                                                                                                                                                   Human; ss; prostate specific cDNA; cytostatic; immunostimulant; gene therapy; cell therapy; vaccine; T-cell epitope; class I major histocompatibility complex allele; MHC; prostate cancer; tumour; antigen presenting cell.
       CTGGGCAGTCTTGCACATGAGATGGGGCTGGTCTGATCTCAGCACTC
                                                                                                                                                                                                                                       Human prostate specific cDNA P80/P704P.
                                                                                                             CATAGITICIGIGCTAGIGGACCGI 385
                                                                                                                        2000US-0054810.
2000US-00568100.
2000US-00597037.
2000US-00697737.
2000US-0069783.
2000US-00636215.
2000US-00657279.
2000US-0067279.
2000US-00678166.
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97US-00904804.
98US-00020955.
98US-00115453.
98US-00159812.
99US-00283149.
99US-00352616.
99US-00439313.
99US-00439313.
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09-FEB-2001; 2001US-00780669.
09-MAY-2001; 2001US-00852911.
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2001US-00012896.
2002US-00144678.
                                                                                                                                                                               ADB13517 standard; cDNA; 385
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                                                                                                                                                                                                                    (first entry)
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09-AUG-2000;
29-AUG-2000;
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09-MAY-2000;
12-MAY-2000;
13-JUN-2000;
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09-NOV-2000;
                                                                                                                                                                                                                                                                                                       Homo sapiens.
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18-NOV-1999;
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TGTGCTGTGCTGGAGATTCACTTTTGAGAGATTCTCCTCTGAGACCTGATCTTTAGAGG

CTGGGCAGTCTTGCACATGAGATGGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG 241 criegical critical caracteristical critical
240

120 180 180

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Gaps

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100.0%; Score 385; DB 10; Length 385; 100.0%; Pred. No. 1.8e-117; ive 0; Mismatches 0; Indels 0.

Best Local Similarity 100. Matches 385; Conservative

Query Match

1 ACTACACACTCCACTTGCCCTTGTGAGACACTTTGTCCCAGCACTTTAGGAATGCTGA

1 ACTACACACACTCCACTTGCCCTTGTGAGACACTTTTGTCCCAGCACTTTAGGAATGCTGA

121 CCCTTTTAAAAAAGGGGACTTGCTTAAAAAAGAAGTCTAGCCACGATTGTGTAGAGCAGC 121 cccrrrraaaaaggggacrrgcrraaaaaaagagcagccacgarrgrgraaggcagc

GGTCGGACCAGCCACATCTCATGTGCAAGATTGCCCAGCAGACATCAGGTCTGAGAGTTC

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The invention relates to an isolated polypeptide comprising no more than 1-542 amino acids of ADB13563 comprising a sequence ADB148187. The peptides comprise a fragment ADB1363 of that contain naturally processed comprises a fragment ADB1363 of that contain naturally processed 7-cell epitopes for 3 class I major histocompatibility complex (MHC) alleles . ADB13653 is a polypeptide encoded by a human prostate specific CDNA, one of 648 disclosed as mew. Also included are nucleic acids in conding the proteins and peptides, expression vectors, a host cell transformed with the vector, an isolated antibody (or antigen binding fragment) that specifically binds to the protein or peptide, detecting fragment) that specifically binds to the protein or peptide beta the protein or appearing as ADB1358, detecting the amount of polypeptide that binds to the agent and comparing the amount of polypeptide that binds to the agent and comparing the amount of polypeptide to a predetermine duting appearing as peptides or protein or poptides or a tumour protein comprising contacting T cells with the apptides or petide to comprising contacting T cells with the peptides or unclain a patient and treating prostate cancer in a patient comprising contacting from a prient with the peptides or antigen presenting cells to the patient. The peptides (or an oligonaclectide (from a patient with the peptides or antigen presenting cells to the patient. The peptides (or an oligonaclectide contacting cells expressing the nucleic acids encoding, or antigen-presenting cells expressing the nucleic acids encoding the contact and administering the peptides, antigen presenting cells expressing the nucleic acids encoding to a cancer in a patient. The peptides (or an oligonaclectide or simulate or expand T cells specific for a tumour protein or treat or simulate or expand T cells specific for a tumour protein or treat or estimulate or expand T cells specific for a tumour protein or the petides, antibodes, tailon proteins, T cell populations or treat or prosta
                                                                                            New isolated polypeptide for use in a vaccine for stimulating an immune response, or for treating or diagnosis cancer, preferably prostate
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Kalos
                                            WPI; 2003-756193/71
Stolk JA,
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Search completed: December 31, 2006, 12:54:17 Job time : 300.256 secs

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PP 25-FEB-1998 JP 1998537008
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PR 25-FEB-1999 US 08/904809 PR 25-FEB-1999 US 08/904809 PR 25-FEB-1998 US 09/020747
PI JIANGCHUN XU,DAVIN C DILLON
PC GOIN33/54, GGIN33/577, C07K16/30, A61K39/395, A61K47/48, C12Q1/68, PC GOIN33/543
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AL512624 Human chr
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AL52819 Homo sapi
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1 (bases 1 to 385)
Xu, J. and Dillon, D.C.
Compounds for immunodiagnosis of prostate cancer and
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                   GenCore version 5.1.9 (c) 1993 - 2006 Biocceleration Ltd.
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                    sapiens (human)'
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Xu,J., Dillon,D.C. and Mitcham,J.L.
Compounds for immunotherapy of prostate
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                       /organism='Homo
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Corixa Corporation; Seattle, WA
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1 (bases 1 to 388)

Dillon, D.C., Harlocker, S.L., Yuqiu, J., Xu, J. and Mitcham, J.L. Compounds for immunotherapy and diagnosis of prostate cancer and methods for their use Patent: JP 2002520054-A 67 09-JUL-2002;

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Unclassified.
1 (bases 1 to 385)
Xu,J. and Dillon, D.C.
Compounds for immunotherapy of prostate their use
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Corixa Corporation; Seattle, WA
Location/Qualifiers
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Sequence 67 from patent US 6613872.
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/wol_type="genomic DNA"
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/mol_type="genomic DNA"
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Best Local Similarity 100.
Matches 385; Conservative
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Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,

Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,

Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,

Hepler,W.T. and Henderson,R.A.

Compositions and methods for the therapy and diagnosis of prostate
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100.0%; Pred. No. 3.8e-117;
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Corixa Corporation; Seattle, WA
Location/Qualifiers
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Sequence 67 from patent US 6620922.
AR399919

    .385
    /organism="unknown"
    /mol_type="genomic DNA"
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Witcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.W., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,
Hepler,W.T. and Henderson,R.A.
Compositions and methods for the therapy and diagnosis of prostate
cancer
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Sequence 67 from patent US 6759515.
AR563566
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Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,

Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,

Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,

Hepler,W.T. and Henderson,R.A.

Compositions and methods for the therapy and diagnosis of pr
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Corixa Corporation; Seattle, WA;

    .385
    /organism="unknown"
    /mol_type="genomic DNA"

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Sequence 67 from patent
AR405186
AR405186.1 GI:40154023
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Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,

Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,

Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,

Hepler,W.T. and Henderson,R.A.

Compositions and methods for the therapy and diagnosis of prostate
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Corixa Corporation; Seattle, WA
Location/Qualifiers
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Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Xalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H., Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W., Hepler,W.T. and Henderson,R.A.
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   06-JUL-2004;
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Sequence 67 from patent US 6800746.
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Corixa Corporation; Seattle,
Location/Qualifiers
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1 (bases 1 to 385)
Xu,J. and Dillon,D.C.
Compounds for immunodiagnosis of prostate cancer and methods for
                        TGTGCTGTGCTGGAGATTCACTTTTGAGAGATTCTCCTCTGAGAGCCTGATCTTTAGAGG
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Corixa Corporation; Seattle, WA
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Sequence 67 from patent US 6894146.
AR656711. GI:67589779
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Sequence 67 from patent US 6887660.
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/organism="unknown"
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1 (bases I to 385)
Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,
Hepler,W.T. and Henderson,R.A.
Compositions and methods for the therapy and diagnosis of prostate cancer
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Corixa Corporation; Seattle, WA
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18.2 559 2 11 18.2 903 14 18.2 674 14	18.0 315 BF991089	7 424 11 AQ426007 740 14 AQ98047 576 11 B81464 8 489 7 BE159477	17.8 517 11 AQ402468 17.8 889 13 CZ461627 17.7 556 9 DB045159	17.7 593 1 AV688475	17.6 623 14 AG079180 17.6 661 14 AG054439	17.5 654 14 AG03794	17.2 242 10 DW439328	587 11 AQS44044 9 521 11 AQS45108	16.8 881 13 CZ458695 CZ458695	ALIGNMENTS	DB045159 TESTI2 Homo sapiens cDNA clone TEST12033322 5', mRNA	sequence. DB045159 DB045159.1 GI:82061582	Homo sapiens (human) Homo sapiens	<pre>Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae; Homo.</pre>	bs6) matsu.A., Suzuki,Y., Ota,T., Nishikawa,T., mamwo.Co,J., Sekine,M., Tsuritani,K., Wakaguri,H., mma,T., Salto,K., Isono,Y., Irie,R., Kuahida,N.,	Yoneyama,I., Ureuka,K., Kanda,K., IOKOI,I., Kohdu,h., Wagarsuma,M., Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A., Tanase T. Nagai,K. Kikuchi H. Nakai,K. Isocai,T. and Sudano.S.	Diversification of Transcriptional Modulation: Large-scale Identification and Characterization of Putative Alternative	Promoters or human Genes Genome Res. 16 (1), 55-65 (2006) 14344560	Contact: Takao Isogai FLJ Project (HRI Team) Helix Research Institute	2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan Tel: 81-438-52-3975	Fax: 81-438-52-3986 Email: flj-cdna@mifty.com NRDO human cDNA project (New Energy and Industrial Technology	Developmental Organization, Japan); cDNA library construction: Helix Research Institute (HRI); 5'-end one pass sequencing: HRI, Research Association for Biotechnology (RAB) and Biotechnology	Center, National Institute of Technology and Evaluation; 3'-end one pass sequencing: RAD	
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5.1.9 Biocceleration Ltd.		ch time 3086.06 Seconds : alignments) ! Million cell updates/sec	0	tttctgtgctagtggaccgt 385			96473596								y chance to have a he result being printed, distribution.		Description	DB045159 DB045159	CD251924 AGENCOURT DN920910 MCF7RNAL2 BC063888 Homo sabi	BX649118 Homo sapi DA554900 DA554900	BQ068886 AGENCOURT CD251853 AGENCOURT AG106788 Pan trod	EX649118 Homo sapi AG065887 Pan trogl AG094252 Pan trogl	CR748036 CR748036 AQ784117 HS 3034 B	DAGE STATE OF THE
GenCore version 5.1.9 Copyright (c) 1993 - 2006 Bioccele	search, using sw model	31, 2006, 12:14:13 ; Searc (without 6976.201		cacactccacttgc	TITY NUC p 10.0 , Gapext 1.0	8236798 seqs, 27959665780 residues	satisfying chosen parameters:	h: 0 h: 2000000000	Minimum Match 0% Maximum Match 100% Listing first 45 summaries	* 500 11	9D_est4:* 9D_est4:* 9D_est5:*	gb_htc:* gb_est2:* gb_est7:*	gb_est9:* gb_est9:* gb_gss]:*	95-982: 95-983: 95-983: 95-9884:	number of results predicted has considered to the score of the analysis of the total score	SUMMARIES	y h Length DB ID	556 9	861 491 5483	553 6098 6098 6098 6098	986 3 873 5 660 14	6098 6 628 14 704 14	861 8 527 11	0 697 4 BX954640 0 1137 3 BU507892 8 863 11 AQ741520
Ö	OM nucleic - nucleic	Run on: December	US BCOre: 38	 	Scoring table: IDENTITY Gapop 10	Searched: 48236	Total number of hits	Minimum DB seq length: Maximum DB seq length:	Post-processing: Mini Maxi List	ES.	4 G W 4 N			1 C C 4	s er	æ	Result Query No. Score Match	312.8 81	3 112.4 29 4 111.8 29 5 107.4 27	101.8 26 100.8 26	95 24 93.4 24 84 2 21	11 83.8 21 12 77.4 20 13 74.4 19	14 74.2 19 15 73.6 19	(1) (3) 19.0 (2) 13 19.0 (2) 18 73 19.0 (2) 19 72.2 18.8

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Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llni.gov
Plate: LLCM2037 row: j column: 18
High quality sequence stop: 751.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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1 (bases 1 to 986)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                  Gaps
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                                                                                                                 DB 9; Length 556;
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                                                                                                                 81.2%; Score 312.8; DB 9;
92.4%; Pred. No. 4.2e-83;
iive 0; Mismatches 27;
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/tissue type="neuroblastoma, cell line"
/lab host="HINDB (phage-resistant)"
/lab host="HINDB (phage-resistant)"
/clone_lib="NIH_MGG_47"
/note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/KhoI sites using the following 5'
adaptor: GGCACGG(G). Size-selected by Ling Hong in
the laboratory of Gerald M. Rubin (University of
california, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleo:
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                     Length 986;
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Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 RM10A07 Bethesda, MD 20892
Email: Capbbs-remail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
                                                                                                                                                                                                                                                                                                                                                                        Score 231.8; DB 3;
Pred. No. 1.6e-58;
0; Mismatches 32;
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AGENCOURT 14204354 NIH MGC_180 Hoi
IMAGE:30383087 5', mRNA sequence.
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88.0%;
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1 (bases 1 to 861)
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Plate: NDAM446 row: f column: 24

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Frammaria, Juniora, Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shemmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haseh, F., Diatchenko, L., Marusina, K., Earmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Wodin, F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Wodin, J.S., Loquellano, N.A., Peters, G.J., Abramson, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Willalon, D.K., Muzhy, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Butterfield, Y.S., Krzywinski, M.I., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Schmutz, J., Myers, R.M., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A., Schein, J.E., Jones, S.J. and Marra, M.A., Schein, J.E., Jones, S.J. and Marra, M.A., A.M.,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (08-DEC-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
cDNA Library Preparation: Invitrogen Corp
cDNA Library Prayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
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90.2%;
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                                                                                                                                                                                                Query Match
Best Local Similarity 90.2<sup>†</sup>
Matches 119; Conservative
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                                              See http
details.'
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                                                                  1. 861

(organism="Momo sapiens"

/mol_type="mRNA"

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MCF7RNAL28P21TR Human MCF7 breast cancer cell line near full length normalized library (MCF7_EST) Homo sapiens cDNA clone MCF7_RNA_L_28_P21, mRNA sequence.
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1 (bases 1 to 491).

Volik, S. V., Raphael, B. J., Huang, G. -Q., Murnane, J., Brebner, J. H., Bajsarowicz, K., Paris, P., Tao, Q., Kowbel, D., Lapuk, A.V., Kuo, W.-L., Shagin, D. A., Shagina, I. A., Magrane, G., Gray, J. W., Jan, F. -C., de Jong, P., Pevraer, P. and Collins, C.

Decoding the genomic architecture and high throughput detection of fusion transcripts in breast cancer cell lines: implications for a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       272 TCTGATCTCAGCACTCCTTAGTCTGCTTGCCTCCCAGGGCCCCAGGCCTGGCCACCT 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       619
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Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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/clone_lib="Human MCF7 breast cancer cell line near full
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 560 TCTGATCTCAGCACTCCTTAGTCTGCTTGCCTCTCCCAGGGCCCCAGCCTGGCCACACCT
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Pred. No. 2e-22;
0; Mismatches 1; Indels 0
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UCSF Box 0808, San Francisco, CA 94143-0808, USA
Tel: 415 502 7067
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Email: svolik@cc.ucsf.edu
Seq primer: SP6 5'-ATTTAGGTGACACTATAGAATAC-3'
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
mol_type="mRNA"
|/db_xref="taxon:9606"
|/dlone="MCF7_RNA_L_28_P21"
|/sex="female"
High quality sequence stop: 7 Location/Qualifiers
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Unpublished (2005)
Contact: Volik SV
Colin Collins' lab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Library."
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Matches 113; Conservative
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                                         FEATURES
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MCF7 breast cancer cell line by Evrogen JSC. (http://www.evrogen.com) using their standard procedure. See http://shark.ucsf.edu/~stas/report_MCF7.pdf for derails."

ö 413 CCTAGCCTGGCCACACATGCTTACAGGGCACTCTTAGATGCCCACACTATAGCTGCCGTG 472 314 CCCAGCCTGGCCACCTGCTTACAGGGCACTCTCAGATGCCCATACCATAGTTTCTGTG 373 353 CACATGAGATGGGGCTGGTCTGATGGCAGCACTCCTTANTCTGCTTGCCTCTCCCATGGC 254 CACATGAGATGGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTGCCTCTCCCAGGGC Gaps ö Length 491; Score 111.8; DB 9; Length Pred. No. 2.7e-22; 0; Mismatches 13; Indels

BC063888 11near HTC 09-DEC-2005 Homo sapiens prostate-specific P704P mRNA, mRNA (cDNA clone IMAGE:30389199), with apparent retained intron.

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

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Gaps

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307

FEATURES

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Email: fll-cdna@mifty.com
NEDO human cDNA project (New Energy and Industrial Technology
Developmental Organization, Japan); cDNA library construction:
Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
Research Association for Biotechnology (RAB) and Biotechnology
Center, National Institute of Technology and Evaluation; 3'-end one
pass sequencing: RAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hominidae, Homo.

I (bases 1 to 553)

Kinura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,
Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H.,
Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N.,
Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M.,
Murakwa,K., Ishida,S., Ishibashi,T., Takahashi-Pujii,A.,
Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.
Diversification of Transcriptional Modulation: Large-scale
Identification and Characterization of Putative Alternative
                                                                                                        /tissue type="testis"
/clone_lib="686 (synonym: hlcc3). Vector pSport1_Sfi; host
DH10B; sites SfilA + SfilB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     soss grerrigeacargadargaagergarergaeereageeereeeragreerageerrgeereee 5006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DAS54900 DAS54900 553 bp mRNA linear EST 06-NOV-2005 DAS54900 HCHON2 Homo sapiens cDNA clone HCHON2005010 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: pME18SFL3; primary culture, chondrocytes"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                       248 GICTIGCACATGAGATGGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTGCCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5005 CAGGACCCCAGCCTGGCCACACACGCCACACGGCACTCTCAGGTGCCCACAC 4953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  308 CAGGGCCCCAGCCTGGCCACCTGCTTACAGGGCACTCTCAGATGCCCATAC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FLJ Project (Hr. Team)
Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
Tel: 81-438-52-3975
                                                                                                                                                                                                                                                                                                           Length 6098;
                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                           DB 6;
                                                                                                                                                                                                                                                                                                        26.4%; Score 101.8; DB 6 93.8%; Pred. No. 5.4e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cell_type="chondrocytes (HC)"
/clone_lib="HCHON2"
/mol_type="mRNA"
/db_xref="RZD0:DKFZp686J0529Q"
/db_xref="taxon:9606"
/clone="DKFZp686J0529"
                                                                                                                                                                                                                          /note="putative transcript"
                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genome Res. 16 (1), 55-65 (2006)
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/db_xref="taxon:9606"
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                                                                                                                                                                                               /dev stage="adult"
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DA554900.1 GI:80884861
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fax: 81-438-52-3986
                                                                                                                                                                                                                                                                                                                                                                     Conservative
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nes 106; Conserv
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PUBMED
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DA554900
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SOURCE
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Homo sapiens mRNA; CDNA DKFZp686J0529 (from clone DKFZp686J0529).
BX649118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3936 TCCCAGCACTCCTTAGTCTGCTTTGCCTCTCCCAGGCCCCCAGCCTGGCCACCTGCTTA 3995
                             info@bcgsc.bc.ca
Martin Hirst, Thomas Zeng, Ryan Morin, Michelle Moksa, Johnson
Pang, Diana Mah, Jing Wang, Kieth Fichter, Eric Chuah, Allen
Peng, Diana Mah, Jing Wang, Kieth Fichter, Eric Chuah, Allen
Delaney, Rob Kirkpatrick, Agnes Baross, Sarah Barber, Mabel
Brown-John, Steve S. Chand, William Chow, Ryan Babakaiff, Dave
Wong, Corey Matsuo, Jaclyn Beland, Susan Gibson, Luis delRio, Ruth
Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
Kim MacDonald, Mike R. Mayo, Josh Moran, Diana Palmquist, JR
Santos, Duane Smailus, Jeff Stott, Miranda Tsai, George Yang,
Jacquie Schein, Asim Siddiqui, Steven Jones, Rob Holt, Marco Marra.
                                                                                                                                                                                                                                                                                                                                           Clone distribution: MGC clone distribution information can be found
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     277 TCTCAGCACTCCTTAGTCTGCCTTCCCCAGGCCCCCAGCCTGGCCACCTGCTTA 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 6098)

Bahr,A., Lauber,J., Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and Wiemann,S.

The German cDNA Consortium
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 141 Row: o Column: 10
This clone has the following problem: retained intron.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (20-JAN-2005) MIDS, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERMANY Clone From S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKF2); Email s.wiemann@dkfz-heidelberg.de; sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing consortium of the German Genome Project.
This clone (DKFZp68640529) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany. Please contact RZPD for ordering:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      337 CAGGGCACTCTCAGATGCCCATACCATAGTTTCTGTGCTAGTGGACGGT 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 5483;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 6;
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     Cancer Agency, Vancouver, BC, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note="Vector: pCMV-SPORT6.1"
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99.1%; Pred. No. 1...
... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
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/organism="Homo sapiens"
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Homo sapiens
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Matches 108; Conservative
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RESULT 6 HSM809270/c

ò 8 ઠે 셤 DEFINITION ACCESSION

LOCUS

VERSION KEYWORDS SOURCE ORGANISM

TITLE JOURNAL

COMMENT

REFERENCE AUTHORS CONSRTM source

FEATURES

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EST 22-MAY-2003
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                                                              261 ATGGCCAGGCTTCTTTTTGAGCAAGTCCCCTTTTTGAAGAGGGGAACTCTGGGAACTGA 320
                                                                                                                         TCTTTAGAGGCTGGGCAGTCTTGCACATGAGATGGGGCTGGTCTGATCTCAGCACTCCTT 290
                                                                                                                                                           Hominidae, Homo.

Is I (bases 1 to 873)

Is National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH

Bldg. 31 Kml0AO' Bethesda, MD 20892

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Michael Brownstein

CDNA Library Preparation: Invitrogen Corp

CONA Library Preparation: Invitrogen Corp

CONA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: NDAM446 row: e column: 23

High quality sequence stop: 540.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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         171 GTAGAGCAGCTGTGCTGTGCAGATTCACTTTTGAGAGAGTTCTCCTCTGAGACCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             272 TCTGATCTCAGCACTCCTTAGTCTGCTTGCCTCCCAGGGCCCCAGGCCTGGCCACCT
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AGENCOURT 14206078 NIH_MGC_180 Homo sapiens cDNA clone IMAGE33383062 5', mRNĀ sequence.
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Pred. No. 1.1e-16;
0; Mismatches 6;
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CD251853.1 GI:31012319
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il Similarity 93.9%;
108; Conservative
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Homo sapiens
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Matches 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue type="neuroblastoma, cell line"
/lab_host="nH10B (phage-resistant)"
/lab_host="nH10B (phage-resistant)"
/lab_host="nH10B (phage-resistant)"
/clone_lib="NH1 MGG-47"
/note="Organ: brain; Vector: pOTB7; Site 1: Xho1; Site_2:
ECORI; cDNA made by oligo-dT priming. DIrectionally
cloned into BcoRI/KhoI sites using the following 5'
adaptor: GGACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
california, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                    BQ068866 986 bp mRNA linear EST 02-APR-2002 AGENCOURT 6740305 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:5802737 5', mRNA sequence.
BQ068886
                                                                 ö
                                                                                                                            299
                                                                                                                                                                                                                                   51 GGAATGCTGAGGTCGGACCACACCTCTCATGTGCAAGATTGCCCAGCAGACATCAGGT .110
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
DNA Sequencing Dy: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image-llnl.gov
Plate: LLCM2037 row; j column: 18
High quality sequence stop: 751.
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                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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   Length 553;
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                                                              Indels
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   Score 100.8; DB 9;
Pred. No. 5.8e-19;
0; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 95; DB 3; I
Pred. No. 3.8e-17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5802737"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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26.2%;
90.0%;
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1 (bases 1 to 986)
                               Best Local Similarity 90.0 Matches 108; Conservative
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Best Local Similarity 65.1
Matches 157; Conservative
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      Query Match
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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
JOURNAL
COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                        RESULT 8
BQ068886
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Hominidae, Homo.

1 (bases 1 to 6098)

2 Bahr, A. Lauber, J., Mewes, H.W., Weil, B., Amid, C., Osanger, A.,

1 Pobo, G., Han, M. and Wiemann, S.

2 Pobo, G., Han, M. and Wiemann, S.

2 The German CDNA Consortium

2 Direct Submission

3 Submitted (10-13M-2005) MIPS, Ingolstaedter Landstr. 1, D-85764

Neuherberg, GERMANY

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer

Research Center (DKF2); Banil s. wiemann@dkfz-heidelberg. de;

sequenced by Qiagen (Hilden/Germany) within the CDNA sequencing

consortium of the German Genome Project.

This clone (DKF2p6860529) is available at the RZPD Deutsches

Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.

Please conteact RZPD for ordering:

thtp://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp686J0529

Further information about the clone and the sequencing project is

available at http://www.rzpd.de/cgi-bin/projects/cdna/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suchiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, WL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170) Clones are derived from the chimpanzee BAC library PTB This BAC end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGU55887 628 bp DNA linear GSS 03-NOV-2001
Pan troglodytes DNA, clone: PTB-055G12.F, genomic survey sequence.
AG065887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3697 caccectradreciderrecerenteces de accecado es estas caractes en estas de contradades de constantes                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 283 CACTCCTTAGTCTGCTTGCCTCTCCCAGGGCCCCAGGCCTGGCCACACCTGCTTACAGGGC
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
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Totoki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of Library PTB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 6098;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12; Indels
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Pred. No. 1.5e-13;
0; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="putative transcript"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
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AG065887/c
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SOURCE
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Homo sapiens mRNA; cDNA DKFZp686J0529 (from clone DKFZp686J0529).
BX649118
BX649118.1 GI:34368290
HTC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (102-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimpses@ger.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  300 GCCTCTCCCAGGGCCCCAGCCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCCATA 359
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                                                                 AG106788 660 bp DNA linear GSS 03-NOV-200
Pan troglodytes DNA, clone: PTB-111G14.R, genomic survey sequence.
                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
Hominidae, Pan.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21.9%; Score 84.2; DB 14; Length 660; 73.8%; Pred. No. 6.4e-14; ive 0; Mismatches 38; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
                                                                                                                                                                                                                                                                                                                                                                                                                Fujiyama,A., Hattori,M., Toyoda,A., 'Totoki,Y., Watanabe,H. and Sakaki,Y. BAC end sequences of Library PTB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               360 CCATAGITICIGIGCIAGIGGACCG 384
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                                                                                                                                                                                                                               Pan troglodytes (chimpanzee)
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R.Site 1 : SacI
R.Site 2 : Sart
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Homo sapiens
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Best Local Similarity
Matches 90; Conserv
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Pujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (02-AUG-2001) Asso Fujiyama, The Institute of Physical
and Chemical Research (RIXEN), Genomic Sciences Center (SSC);
1-7-22 Suchiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:sla145-S03-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                               1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSS 03-NOV-2001
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Pan troglodytes DNA, clone: PTB-094P10.R, genomic survey sequence.
AG094252
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
was generated during the R&D process and may have higher chance
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                                                                                                                                                                   1. 628
/organism="Pan troglodytes"
/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-055G12.F"
/sex="manle"
/cell type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                    Length 628;
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                                                                                                                                                                                                                                                                                                                                                                    Query Match 20.1%; Score 77.4; DB 14;
Best Local Similarity 74.2%; Pred. No. 7.2e-12;
Matches 115; Conservative 0; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        351 ATGCCCATACCATAGTTTCTGTGCTAGTGGACCGT 385
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Pan troglodytes
                                                                                          Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI.
                                                      Sequencing: -21M13
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R.Site 1 : SacI
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                clone tracking errors.
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CR748036 CR748036 B61 bp mRNA linear EST 21-DEC-2004 CR748036 Homo sapiens library (Ebert L) Homo sapiens cDNA clone IMAGP998D104117 ; IMAGE:1623129 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini;
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Ebert, L., Heil, O., Hennig, S., Korn, B., Neubert, P., Partsch, E.
Peters, M., Radelof, U. and Schneider, D.
IM.A.G.E. CDNA Clone Collection
Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Inge Arlart

READ Doutsches Ressourcenzentrum fuer Genomforschung GmbH

Heubnerweg 6, D-14059 Berlin, Germany

Email: www.rzpd.de

REZPD; IMAGP998D104117.

RZPDIIB; I.M.A.G.E. CDNA Clone Collection;

Contact: Inge Arlart
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Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 100
Fax: +49 30 32639 111
www.rzpd.de
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                                                                                                                                                                                                                                                                          ch 19.3%; Score 74.4; DB 14; Length 704; 1 Similarity 77.6%; Pred. No. 6e-11; 90; Conservative 0; Mismatches 26; Indels 0
                                                                                                                                              /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 861;
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19.3%; Score 74.2; DB 8; Length 86
Best Local Similarity 72.9%; Pred. No. 7.3e-11;
Matches 113; Conservative 0; Mismatches 33; Indels
organism="Pan troglodytes"

    .861
    /organism="Homo sapiens"

                      /mol type="genomic DNA"
/db xref="taxon:9598"
/clone="PTB-094P10.R"
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CR748036.1 GI:51661862
                                                                                                                           /sex="male"
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us-09-232-880-67.rst

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Hominidae; Homo.
1 (bases 1 to 527)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
McRiler,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
                                                                                                                                                                                                                   AQ784117 527 bp DNA linear GSS 03-AUG-1999 HS_3034_B1_A11_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3034 Col=21 Row=B, genomic survey
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-368
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Jate: 3034 row: B column: 21
Seg primer: T
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/clone lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
B-Coli DH108
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19.1%; Score 73.6; DB 11; Length 527;
Best Local Similarity 78.6%; Pred. No. 9.8e-11;
Matches 88; Conservative 0; Mismatches 24; Indels 0;
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|mol_trype="genomic DNA"
|db_xref="taxon:9606"
|clone="plate=3034 Col=21 Row=B"
                                                                   355 ----CCATACCATAGTTTCTGTGCTAGTGGACCGT 385
                                                                                         High quality sequence stop: 527.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                          AQ784117
AQ784117.1 GI:5691741
                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (human)
Homo sapiens
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AQ784117
LOCUS
DEFINITION
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PUBMED
COMMENT
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AUTHORS
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Search completed: December 31, 2006, 19:30:49 Job time : 3091.06 secs

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LENGTH: 385
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| FMC Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
| FMC Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
| FMC Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
| FMC Celerra_SIDS3/ptodata/2/pubpna/US09_PUBCOMB.seq:*
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| FMC Celerra_SIDS3/ptodata/2/pubpna/US118_PUBCOMB.seq:*
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Sequence 1036, Ap
Sequence 11258, A
Sequence 701, App
                                                                                                                         December 31, 2006, 12:22:01 ; Search time 613.045 Seconds (without alignments) 7716.790 Million cell updates/sec
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-10-198-846-11258
US-11-234-786-701
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US-09-822-827-67
US-09-232-880-67
US-09-895-793-67
US-09-895-194-67
US-10-012-896-67
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US-10-688-838-67
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Sequence 8224, Ap. Sequence 289560, Sequence 289561, Sequence 289561, Sequence 289562, Sequence 289562, Sequence 36451, Sequence 979860, Sequence 979860, Sequence 979861, Sequence 979861, Sequence 979861, Sequence 16453, Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. Sequence 21826, A. S
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US-09-759-143-701

US-09-180-69-701

US-09-895-793-701

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US-10-12-896-701

US-10-12-896-701

US-10-12-896-701

US-10-18-678A-701

US-10-18-84-025-701

US-10-18-84-025-701

US-09-925-065A-289561

US-09-925-065A-289561

US-09-925-065A-289561

US-09-925-065A-289561

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US-10-301-480-366452

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AL I GNMENTS

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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427023
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CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSEQ for Windows Version 3.0
Sequence 67, Application US/09759143
Patent No. US2002022248A1
GENERAL INFORMATION:
                                                                                                                                       Harlocker, Susan L.
Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
                                                                     Xu, Jiangchun
Dillon, Davin C.
Mitcham, Jennifer L.
                                                                                                                                                                                                                                                                                  Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
Li, Samuel
                                                                                                                                                                                                                                                                                                                                                                                                             Wang, Aijun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapien
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1 ACTACACACACTCCACTTGCCCTTGTGAGACACTTTGTCCCCAGCACTTTAGGAATGCTGA 60

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Query Match 100.0%; Score 385; DB 3; L
Best Local Similarity 100.0%; Pred. No. 2.2e-126;
Matches 385; Conservative 0; Mismatches 0;
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
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nucleic acid
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US-09-030-606-67
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                                                                                                        CCCTTTTAAAAAAGGGGACTTGCTTAAAAAGAAGTCTAGCCACGATTGTGTAGAGCAGC 180
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CCCTTTTAAAAAAGGGGGCTTTCTTAAAAAAGAAGTCTAGCCACGATTGTGTAGAGCAGC
                                                                                                                                                                    TGTGCTGTGCTGGAGATTCACTTTTGAGAGATTCTCCTCTGAGACCTGATCTTTAGAGG
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                                               GGTCGGACCAGCCACCATCTCATGTGCAAGATTGCCCAGCAGACATCAGGTCTGAGAGTTC
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
TITLE REFERENCE: 210121.427C24
CURRENT APPLICATION NHBER: US/09/780,669
CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
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Best Local Similarity 100.0%; Pred. No. 2.2e-126;
Matches 385; Conservative 0; Mismatches 0;
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Patent No. US20020051977A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xu, Jiangchun
Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
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Henderson, Robert A.
Kalos, Michael D.
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McNeill, Patricia D.
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Skeiky, Yasir A.W.
Hepler, William
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Vedvick, Thomas S.
Carter, Darrick
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Retter, Marc W.
Stolk, John A.
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ORGANISM: Homo sapien
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US-09-780-669-67
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SEQ ID NO 67
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APPLICANT:
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Sequence 67, Application US/09030606
| Patent No. US20020081580A1
| CENERAL INPOWATION:
| APPLICANT: Xu, Jaingchun |
| APPLICANT: Xu, Jaingchun |
| TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHODS FOR RESPONDENCE ADDRESS:
| ADDRESSEE: SEED and BERRY LiP |
| STREET: 6300 Columbia Center, 701 Fifth Avenue |
| CITY: Seatile |
| STATE: WA
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61 GGTCGGACCAGCCACATCTCATGTGCAAGATTGCCCAGCAGACATCAGGTCTGAGAGTTC
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                                                                                                     TGTGCTGTGCTGGAGATTCACTTTTGAGAGTTCTCCTCTGAGACCTGATCTTTAGAGG
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                                                                          CCCITITIAAAAAAGGGGACITGCTTAAAAAAGAAGTCTAGCCACGATTGTGTAGAGCAGC
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/030,606
FILING DATE: 25-FEB-1998
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Patent No. U520020090372A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND
TITLE OF INVENTION: COMPOUNDS FOR THEIR USE
FILE REPERENCE: 210121.427C4
CURRENT APPLICATION NUMBER: US/09/115,453B
CURRENT APPLICATION NUMBER: US/09/115,453B
CURRENT PILING DATE: 1998-07-14
NUMBER OF SEQ ID NOS: 228
SOFTWARE: FastSEQ for Windows Version 3.0
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Publication No. US20020182596A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF
TITLE OF INVENTION: PROSTATE CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.428C6
CURRENT APPLICATION NUMBER: US/09/232,880
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Best Local Similarity 100.0%; Pred. No. 2.2e-126;
Matches 385; Conservative 0; Mismatches 0;
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ORGANISM: Homo sapien
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US-09-115-453-67
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US-09-232-880-67
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                            ACTACACACACTCCACTTGCCCTTGTGAGACACTTTGTCCCCAGCACTTTAGGAATGCTGA
                                                                                        GGTCGGACCAGCCACATCTCATGTGCAAGATTGCCCAGCAGACATCAGGTCTGAGAGTTC
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Patent No. US20020001680A1
GENERAL INFORMATION:
APPLICAMT: W. Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210.21.534C1
CURRENT APPLICATION NUMBER: US/09/822,827
CURRENT PILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSEQ for Windows Version 3.0
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; ORGANISM: Homo sapien
US-09-822-827-67
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                                                                                                                                                               100.0%; Score 385; DB 3; Length 385; 100.0%; Pred. No. 2.2e-126; Live 0; Mismatches 0; Indels
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 67
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Skeiky, Yasir A.W.
Hepler, William T.
Henderson, Robert A.
Hural, John
McWelll, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
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                                                                                                                                                                 Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 385; Conservative C
                                                                                            ; TYPE: DNA
; ORGANISM: Homo sapien
US-09-895-793-67
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                                                                            LENGTH: 385
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER FILE REFERENCE: 21012.1.5342.
CURRENT APPLICATION NUMBER: US/09/895,793
                                                                                                                                                                     Length 385
                                                                                                                                                                                                     0; Indels
                                                                                                                                                                     100.0%; Score 385; DB 3; I
100.0%; Pred. No. 2.2e-126;
ive 0; Mismatches 0;
                   NUMBER OF SEQ ID NOS: 338
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 67
LENGTH: 385
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McNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
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Publication No. US20020192763A1
GENERAL INFORMATION:
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Glang, Yuqiu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
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Skeiky, Yasir A.W.
Hepler, William T.
Henderson, Robert A.
       CURRENT FILING DATE: 1999-01-15
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Vedvick, Thomas S.
Carter, Darrick
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Best Local Similarity 100.
Matches 385; Conservative
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                                                                                                ; TYPE: DNA
; ORGANISM: Homo sapien
US-09-232-880-67
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APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang Yuqui
APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Retter, Mark
APPLICANT: Retter, Mark
APPLICANT: CONPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.42703
CURRENT APPLICATION NUMBER: US/10/010,940
CURRENT FILING DATE: 2001-12-05
                                                                                                                                                                                                                                                                                                                                                                                Length 385;
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100.0%; Score 385; DB 6; L
Best Local Similarity 100.0%; Pred. No. 2.2e-126;
Matches 385; Conservative 0; Mismatches 0;
FILE REFERENCE: 210121.427C27
CURRENT PAPLICATION NUMBER: US/10/012,896
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 67
LENGTH: 385
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 67
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                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Homo sapiens
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CORGANISM: Homo sapien
US-10-010-940-67
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APPLICANT: Wantanabe, Yoshihiro
APPLICANT: Masgher, Madeleine Joy
APPLICE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
                                                                                                                                                                                                                                                                                                             Length 385;
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                            NUMBER OF SEQ ID NOS: 990
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 67
LENGTH: 385
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Houghton, Raymond L.
Vinals de Bassols, Carlota
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Publication No. US20020183251A1
GENERAL INFORMATION:
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
   2001-06-29
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Vedvick, Thomas S.
Carter, Darrick
Li, Samuel X.
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Hepler, William T.
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                                                                                                                                                                      TYPE: DNA
CORGANISM: Homo sapien
US-09-895-814-67
   CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 385; Conserv
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                                                                       ; DB 7; Length 385; 2.2e-126;
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Publication No. US20030185830A1

GENERAL INFORMATION:

APPLICANT: Xu. Jiangchun

APPLICANT: Stolk, John A.

APPLICANT: Stolk, John A.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

FILE REFERENCE: 210121.477C29

CURRENT APPLICATION NUMBER: US/10/294,025

CURRENT FILING DATE: 2002-11-12

WUMBER OF SEQ ID NOS: 1038

SOFTWARE: FRASERE for Windows Version 3.0

SEQ ID NO 67
                                                                                                                                0; Mismatches
                                                                          100.0%; Score 385;
100.0%; Pred. No. 2
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; ORGANISM: Homo sapiens
US-10-294-025-67
                    US-10-144-678A-67
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                                                                                Gaps
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APPLICANT: Vinals y de Basols, Carlota
APPLICANT: Poy, Teresa M
APPLICANT: Poy, Teresa M
APPLICANT: Pong, Ta
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C28
CURRENT PILLING DATE: 2002-08-12
CURRENT FILING DATE: 2002-08-12
NUMBER OF SEQ ID NOS: 1033
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 67
LENGTH: 385
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                    Length 385;
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                       Score 385; DB 6; L
Pred. No. 2.2e-126;
100.0%; Scc. 100.0%; Pred. No. ...
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McNeill, Patricia D.
Houghton, Raymond L.
Vinals y de Bassols, Carlota
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Hitcham, Jennifer L.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Ralos, Michael D.
APPLICANT: Ratter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel X.
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Skeiky, Yasir A. W.
Hepler, William T.
                       Query Match 100.
Best Local Similarity 100.
Matches 385; Conservative
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ORGANISM: Homo sapiens
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US-10-144-678A-67
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SEQ ID NO 67
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                                                                                                                                            CCTCTCCCAGGCCCCAGCCTGGCCACCTGCTTACAGGGCACTCTCAGATGCCCATAC 360
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                                                                                                                                                                                                                                                                                                              Sequence 67, Application US/10688838
| Publication No. US20040141989A1
| GENERAL INFORMATION:
| APPLICANT: W. Jiangchun
| APPLICANT: Dillon, Davin C.
| TITLE OF INVENTION: COMPGUNDS FOR IMMUNOTHERAPY OF PROSTATE
| TITLE OF INVENTION: COMPGUNDS FOR THEIR USE
| TITLE OF INVENTION: COMPGUNDS FOR IMMUNOTHERAPY OF PROSTATE
| TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
| FILE REFERENCE: 210121.42704
| CURRENT FILING DATE: 2003-10-17
| NUMBER OF SEQ ID NOS: 228
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 67
| LENGTH: 385
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Best Local Similarity 100.0%; Pred. No. 2.2e-126;
Matches 385; Conservative 0; Mismatches 0;
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10S-11-234-786-67
Sequence 67, Application US/11234786
Publication No. US20060024301A1
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ORGANISM: Homo sapiens
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US-10-688-838-67
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TITLE OF INVENTION: PROSTATE-SPECIFIC POLYPEPTIDES AND FUSION
TITLE OF INVENTION: PROSTATE-SPECIFIC POLYPEPTIDES AND FUSION
TITLE OF INVENTION: PROSTATE-SPECIFIC POLYPEPTIDES AND FUSION
FILE REFERENCE: 210121.427031
CURRENT PELICATION NUMBER: US/11/234,786
CURRENT PELICATION NUMBER: US 09/568,857
PRIOR FILING DATE: 2000-05-09
PRIOR PELICATION NUMBER: US 09/536,857
PRIOR PELICATION NUMBER: US 09/483,672
PRIOR PELICATION NUMBER: US 09/483,672
PRIOR PELICATION NUMBER: US 09/483,672
PRIOR PELICATION NUMBER: US 09/439,313
PRIOR PELICATION NUMBER: US 09/352,616
PRIOR PELICATION NUMBER: US 09/252,616
PRIOR PELING DATE: 1999-07-13
PRIOR PELING DATE: 1999-07-13
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PRIOR PELING DATE: 1999-07-15
PRIOR APPLICATION NUMBER: US 09/115,453
PRIOR PELING DATE: 1999-07-15
PRIOR APPLICATION NUMBER: US 09/030,607
PRIOR PELING DATE: 1999-07-15
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                                                                                                               Harlocker, Susan L.
Jiang, Yuqiu
Reed, Steven G.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
Li, Samuel X.
(u, Jiangchun
Dillon, Davin C.
Mitcham, Jennifer 1
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Matches 385; Conservative
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241 CTGGGCAGTCTTGCACATGAGATGGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG 300
                                                                 2342 GGTCAGACCAGCCACATCTCATGTGCAAGATTGCCCAGCAGACATCAGGTCTGAGAGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2282 ACCACACACTCCACTTGCCCTTGTGAGACACTTTGTCCCAGCACTTTAGGAATGCTGA
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                                                                                                                                                                                                                                                    ; Sequence 1036, Application US/10294025
; Publication No. US2003185830A1
; GENERAL INFORMATION:
; APPLICANT: Xu Jungchun A.
; APPLICANT: Xt Jungchun A.
; APPLICANT: Xt Jungchun A.
; APPLICANT: Xt Jungchun A.
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C29
; CURRENT APPLICATION NUMBER: US/10/294,025
; CURRENT FILING DATE: 20022-11-12
; NUMBER OF SEQ ID NOS: 1038
; SOOTWARE: FESTERQ for Windows Version 3.0
; SEQ ID NO 1036
; LENGTH: 3710
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99.2%; Score 381.8; DB 7; Length 3710;
Best Local Similarity 99.5%; Pred. No. 8.4e-125;
Matches 383; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2642 CATAGTTTCTGTGCTAGTGGACCGT 2666
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                                                                                                                        CATAGITICIGIGCIAGIGGACCGI 385
                                                                                                                                               ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-294-025-1036
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US-10-294-025-1036
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Search completed: December 31, 2006, 13:56:03 Job time : 615.045 secs

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Published Applications NA New:*

1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_NEW_PUB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*
                                                                                                                                                                                                                      (without alignments)
6266.684 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                              December 31, 2006, 12:26:03'; Search time 557.33 Seconds
GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3050214 segs, 1077301958 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries
                                                                                                                      OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                   US-09-232-880-107
                                                                                                                                                                                                                                                                                                                   Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Database :
                                                                                                                                                                                                                                                                                                                                                                                 Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                        Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 107, App	Sequence 107, App	Sequence 23190, A	Sequence 104, App	Sequence 22797, A	Sequence 23899, A	Sequence 57286, A	Sequence 215905,	Sequence 237887,	Sequence 46436, A	Sequence 84584, A	Sequence 111891,	Sequence 137395,	Sequence 74, Appl	Sequence 74, Appl	Sequence 349470,	Sequence 432849,	Sequence 371009,	Sequence 454388,	Sequence 4076, Ap	Sequence 1504, Ap	Sequence 4921, Ap
	ΩI	US-11-344-932-107	US-11-349-541-107	US-11-266-748A-23190	US-11-343-797-104	US-11-266-748A-22797	US-11-266-748A-23899	US-11-266-748A-57286	US-11-266-748A-215905	US-11-266-748A-237887	US-11-266-748A-46436	US-11-266-748A-84584	US-11-266-748A-111891	US-11-266-748A-137395	US-11-344-932-74	US-11-349-541-74	US-11-266-748A-349470	US-11-266-748A-432849	US-11-266-748A-371009	US-11-266-748A-454388	US-11-190-172-4076	US-11-301-554-1504	US-11-371-354-4921
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*	Match	100.0	100.0	97.1	97.1	6.96	94.1	76.5	54.4	54.4	48.3	45.3	45.3	45.3	31.8	31.8	31.7	31.7	31.7	31.7	27.6	26.3	26.2
	Score	1621	1621	1574.2	1574.2	1571	1524.8	1240.6	882.2	882.2	783	734.6	734.6	734.6	515	515	514	514	513.6	513.6	447.8	426.8	424
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Sequence 59156, A Sequence 3, Appli	Sequence 3, Appli	Sequence 33, Appl	Sequence 33, Appl	Sequence 2, Appli	Sequence 2, Appli	Sequence 252, App	Sequence 242, App	Sequence 6, Appli	Sequence 380888,	Sequence 464267,	Sequence 224722,	Sequence 246615,	Sequence 398998,	Sequence 470044,	Sequence 84585, A	Sequence 111892,	Sequence 137396,	Sequence 16830, A	Sequence 2253, Ap	Sequence 10189, A	Sequence 11125, A	
US-11-371-354-59156 US-11-344-932-3	0 US-11-349-541-3	US-11-344-932-33	0 US-11-349-541-33	US-11-344-932-2	0 US-11-349-541-2	US-11-344-932-252	US-11-344-932-242	US-10-527-552-6	US-11-266-748A-380888	US-11-266-748A-464267	US-11-266-748A-224722	US-11-266-748A-246615	US-11-266-748A-398998	US-11-266-748A-470044	US-11-266-748A-84585	US-11-266-748A-111892	US-11-266-748A-137396	0 US-11-292-078-16830	0 US-11-292-078-2253	0 US-11-292-078-10189	0 US-11-292-078-11125	
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424	406.6	403.2	403.2	400.2	400.2	275.4	272.4	234.8	189.4	189.4	121.4	121.4	121.4	121.4	104	104	104	81	79.4	76.8	75.6	
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ALIGNMENTS

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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER FILE SPERENCE: 210121.427632 CURRENT APPLICATION NUMBER: US/11/344,932 CURRENT FILING DATE: 2006-02-01 PRIOR APPLICATION NUMBER: 10/144,678 PRIOR PILING DATE: 2002-05-09 PRIOR APPLICATION NUMBER: 10/012,896 PRIOR FILING DATE: 2001-12-10 PRIOR PILING DATE: 2001-12-10 PRIOR FILING DATE: 2001-12-10 PRIOR FILING DATE: 2001-06-29 PRIOR FILING DATE: 2001-06-29 PRIOR FILING DATE: 2001-06-29 PRIOR PILING DATE: 2001-06-99 PRIOR PILING DATE: 2001-06-99 PRIOR PILING DATE: 2001-06-99 PRIOR PILING DATE: 2001-06-99 PRIOR PILING DATE: 2001-06-99 PRIOR PILING DATE: 2001-02-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hural, John
McNeill, Patricia D.
Houghton, Raymond L.
Vinals y de Bassols, Carlota
Foy, Teresa M.
                       Sequence 107, Application US/11344932
Publication No. US20060269532A1
GENERAL INFORMATION:
                                                                                            APPLICANT: Xu, Jiangchun APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Watanabe, Yoshihiro
Meagher, Madeleine Joy
                                                                                                                                                                                                                                                                    Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Skeiky, Yasır A. W.
Hepler, William T.
                                                                                                                                                                                                                                                                                                                                                                                                                              Samuel X.
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US-11-344-932-107
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APPLICANT:
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TITCAAAAGGGATCCITICATAGGAGAACACACTGAGGAGATACTIGAAGAATTTGGATT 1080
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US-11-349-541-107
Sequence 107, Application US/11349541
Fublication No. US20060223129A1
Fublication No. US20060223129A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COAVIN C.
TITLE OF INVENTION: METHODS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND
TITLE OF INVENTION: METHODS FOR THEIR USE
FILE REFERENCE: 210121.428C7
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                                       GAAGGCAGAGTGGTGTAAATCTTTGACGGCACAGATGCCTGTGTGACTCCGGTTCTGAC
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                           GAGCATGGATGATTGGCCAGAAATGAAGAAGAAGTTTGCAGATGTATTTGCAAAGAAGAC
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Pred. No. 4e-304;
Mismatches 0;
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PRIOR APPLICATION NUMBER: 09/759,143
PRIOR FILING DATE: 2001-01.12
PRIOR APPLICATION NUMBER: 09/709,729
PRIOR FILING DATE: 2000-11.09
PRIOR FILING DATE: 2000-10-10
PRIOR PLING DATE: 2000-10-10
PRIOR PLING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: 09/679,426
PRIOR PILING DATE: 2000-00-02
PRIOR PILING DATE: 2000-09-06
Remaining Prior Application data removed . St. NUMBER OF SEC ID NOS: 1033
SOFTWARE: FastSEQ for Windows Version 3.0
SEC ID NO 107
LENGTH: 1621
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100.0%; Pred
0; P
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                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-344-932-107
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Best Local Similarity
Matches 1621; Conserv
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Publication No. US20060134663A1
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Johnston, Partick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
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CURRENT APPLICATION NUMBER: US/11/349,541
CURRENT FILING DATE: 2006-02-06
PRIOR PELLING DATE: 1006-02-06
PRIOR FILING DATE: 1998-07-14
PRIOR FILING DATE: 1998-07-14
PRIOR FILING DATE: 1998-02-25
PRIOR PILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: US 09/020,747
PRIOR APPLICATION NUMBER: US 08/904,809
PRIOR APPLICATION NUMBER: US 08/904,809
PRIOR APPLICATION NUMBER: US 08/904,809
PRIOR APPLICATION NUMBER: US 08/906,596
PRIOR FILING DATE: 1997-02-25
NUMBER OF SEQ ID NOS: 228
SOUTWARE: PRACES FRACES OF WINDOWE VERSION 3.0
                                                                                                                                                                                                                                                                                                                             Query Match
100.0%;
Best Local Similarity 100.0%;
Matches 1621; Conservative 0
                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Homo sapien
US-11-349-541-107
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TITLE OF INVENTION: Methods of Using the Sammer File Reference: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105492.2
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
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PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PATENTIN VETSION 3.3
SEQ ID NO 231990
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; ORGANISM: Homo Sapiens
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Publication No. US20060134663A1
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
ITILE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REPERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
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             APPLICANT: Rubin, Mark A.
APPLICANT: Sreekumar, Arun
TITLE OF INVENTION: Expression Profile of Profile OF INVENTION: Expression Profile of Profile OF INVENTION: Expression Profile of Profile OF INVENTION: BAPLICATION NUMBER: US/11/343,797
CURRENT FILING DATE: 2006-01-31
PRIOR PILING DATE: 2001-08-01
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-11-15
NUMBER: OF SEQ ID NOS: 123
SEQ ID NO 104
LENGTH: 2005
APPLICANT: Chinnaiyan, Arul M.
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.larity 99.7%; Pred. No. 2e-294;
Conservative 0; Mismatches 5; Indels 0
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
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US-11-266-748A-22797
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TITLE OF INVENTION: Transcriptome Microarray Technology and TITLE OF INVENTION: Methods of Using the Same FILE REPERRICE: 55815-0102 (319189)

CURRENT APPLICATION NUMBER: US/11/266,748A

CURRENT FILING DATE: 2005-11-03

PRIOR APPLICATION NUMBER: EP 04105482.6

PRIOR PILING DATE: 2004-11-03

PRIOR PILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105483.4

PRIOR PILING DATE: 2004-11-03

PRIOR PILING DATE: 2004-11-03

PRIOR FILING DATE: 2005-01-16

PRIOR FILING DATE: 2005-07-18

NUMBER OF SEQ ID NOS: 483996

SOFTWARE: PATENTIN VERSION 3.3

SEQ ID NO 23899
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: LOCATION: (143)..(143)

: OTHER INFORMATION: n is a, c,

US-11-266-748A-23899
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Best Local Similarity 98.6%;
Matches 1559; Conservative
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Publication NO. US20060134663A1

Fublication NO. US20060134663A1

Fublication NO. US20060134663A1

APPLICANT: Harkin, Paul

APPLICANT: Johnston, Patrick

APPLICANT: Mulligan, Karl

TITLE OF INVENTION: Transcriptome Microarray Technology and

TITLE OF INVENTION: Methods of Using the Same

FILE REFERENCE: 5815-0102 (319189)

CURRENT APPLICATION NUMBER: US/11/266,748A

CURRENT FILING DATE: 2005-11-03

FRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105479.2
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APPLICANT: ADINATION, PATTICK
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
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                                                                                                                                  5-11-266-748A-215905/c
Sequence 215905, Application US/11266748A
Publication No. US20060134663A1
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
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// LOCATION: (893)

// OTHER INFORMATION: n is a, c, g,

US-11-266-748A-215905
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Best Local Similarity 96.3%
Matches 893; Conservative
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OTHER INFORMATION: n is
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OTHER INFORMATION: n is
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OTHER INFORMATION: n is
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1032 ATCCTTTCATAGGAGAACACAGTGAGGAGATACTTGAAGAATTTGGATTCAGCCGCGAAG 1091
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APPLICANT: Horoxanilon:
APPLICANT: Johnston, Patrick
APPLICANT: Johnston, Patrick
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APPLICANT: Johnston, Patrick
ITILE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: Methods of Using the Same
FILE REPERBENCE: 58815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2004-11-03
FRIOR PILING DATE: 2004-11-03
FRIOR PILING DATE: 2004-11-03
FRIOR PILING DATE: 2004-11-03
FRIOR APPLICATION NUMBER: EP 04105483.4
FRIOR PILING DATE: 2004-11-03
FRIOR APPLICATION NUMBER: EP 04105485.9
FRIOR PILING DATE: 2004-11-03
FRIOR PILING DATE: 2004-11-03
FRIOR PILING DATE: 2004-11-03
FRIOR PILING DATE: 2004-11-03
FRIOR PILING DATE: 2004-11-03
FRIOR PILING DATE: 2005-01-18
FRIOR PILING DATE: 2005-01-18
FRIOR PILING DATE: 2005-07-18
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ORGANISM: Homo Sapiens
FEATURE:
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SEQ ID NO 46436
LENGTH: 958
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  PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
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PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-07-18
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; LOCATION: (948)...(949)
; JOHER INFORMATION: n is a, c, g, or
US-11-266-748A-237887
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NAME/KEY: misc feature
LOCATION: (79) ...(79)
OTHER INFORMATION: n is a, c,
FEATURE:
NAME/KEY: misc_feature
LOCATION: (933) ...(933)
OTHER INFORMATION: n is a, c,
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NAME/KEY: misc feature
LOCATION: (936)..(937)
OTHER INFORMATION: n is a,
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LOCATION: (945)...(945)
OTHER INFORMATION: n is a,
FEATURE:
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Matches 893; Conservative
                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo Sapiens
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: LOCATION: (993)..(993)

: OTHER INFORMATION: n is a, c,

US-11-266-748A-84584
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 84584
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  US20060134663A1
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LOCATION: (822)..(822)
OTHER INFORMATION: n is
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LOCATION: (773)..(773)
OTHER INFORMATION: n is
FEATURE:
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OTHER INFORMATION: n is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo Sapiens
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NAME/KEY: misc feature
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Best Local Similarity
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                                                                                                                                                                          GGACAGCAGATGGGGAATTCATGGCTGTTGGAGCAATAGAACCCCCAGTTCTACGAGCTGC
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                                                                                                                                      7;
                                                                                                 Length 958
                                                                                                                                    Indels
                                                                                                                                      31;
                                                                                               Score 783; DB 8; 1
Pred. No. 3.7e-142;
0; Mismatches 31;
                                        or
                    ; LOCATION: (709)
; OTHER INFORMATION: n is a, c, g,
US-11-266-748A-46436
                                                                                           Query Match
Best Local Similarity 95.8%;
Matches 858; Conservative
NAME/KEY: misc_feature
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RESULT 11 US-11-266-748A-84584 ; Sequence 84584, Application US/11266748A

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GAGGAGCAGGAGGCCCCCCCCCCCCCCCCCCCCCTTAAACACCCCCAGCCATCCCT 1018
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APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
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Pred. No. 8.3e-133;
0; Mismatches 14;
                                                                                                                           TITLE REPERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR PILING DATE: 2005-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-03-14
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45.3%; Score 734.6; DB 8;
Best Local Similarity 97.7%; Pred. No. 8.3e-133;
Matches 798; Conservative 0; Mismatches 14;
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Sequence 11189J, Application US/11266748A
Fublication No. US20060134663AI
FABRICANT: Harkin, Paul
APPLICANT: Harkin, Paul
APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
FILE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: Methods of Using the Same
FILE OF INVENTION: MUMBER: BP 0410549.2
PRIOR PELING DATE: 2004-11-03
PRIOR PELING DATE: 2004-11-03
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805 ACGAAGCCAGAGTGGTGTCAAATCTTTGACGGCACAGATGCCTGTGTGACTCCGGTTCTG 746
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Publication No. US20060269532A1
GENERAL INFORMATION:
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
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Houghton, Raymond L.
Vinals y de Bassols,
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Hepler, William T.
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Vedvick, Thomas
Carter, Darrick
Li, Samuel X.
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Retter, Marc W.
Stolk, John A.
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                                                                                                                                                                                                                                                                            APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REPERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
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                        1496 CATTTATTTACACTCTT-GATTCTACAATGTAGAAAA 1531
                                                   Query Match 45.3%; Score 734.6; DB 8; Best Local Similarity 97.7%; Pred. No. 8.3e-133; Matches 798; Conservative 0; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR PLING DATE: 2004-11-03
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PRIOR FILING DATE: 2004-11-03
PRIOR PRILING DATE: 2004-11-03
PRIOR PRIOR FILING DATE: 2004-11-03
PRIOR PRILING DATE: 2005-03-14
PRIOR PRILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-03-14
                                                                                                                                                                                   Sequence 137395, Application US/11266748A Publication No. US20060134663A1 GENERAL INFORMATION:
APPLICANT: Harkin, Paul
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OTHER INFORMATION: n is a, c, g, or t
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OTHER INFORMATION: n is a,
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LOCATION: (52)..(52)
OTHER INFORMATION: n is
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NAME/KEY: misc_feature
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NAME/KEY: misc_feature
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LENGTH: 924
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GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND
TITLE OF INVENTION: WETHOOS FOR THEIR USE
FILE REFERENCE: 210121:428C7
CURRENT APPLICATION NUMBER: US/11/349,541
CURRENT FILING DATE: 1298-07-14
PRIOR PLING DATE: 1298-07-14
PRIOR PLING DATE: 1998-07-25
PRIOR PLING DATE: 1998-07-25
PRIOR PRILING DATE: 1998-07-25
PRIOR FILING DATE: 1998-00-25
PRIOR FILING DATE: 1998-00-25
PRIOR FILING DATE: 1997-08-01
PRIOR PRILICATION NUMBER: US 08/904,809
PRIOR PRILING DATE: 1997-08-01
PRIOR PRILING DATE: 1997-08-01
PRIOR APPLICATION NUMBER: US 08/904,809
PRIOR PRILING DATE: 1997-08-01
PRIOR PRILING DATE: 1997-08-01
PRIOR PRILING DATE: 1997-08-05
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                                                                                         1276 AAAGAATTACAGACTCTGATTCTACAGTGATGAATTCTAAAAAATGGTTATCATTAG
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31.8%; Score 515; DB 10; Length 537;
Best Local Similarity 98.5%; Pred. No. 2.1e-90;
Matches 529; Conservative 0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 74, Application US/11349541; Publication No. US20060223129A1; GENERAL INFORMATION:
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; OTHER INFORMATION: n = A,T,C or G
US-11-349-541-74
                                                      1456 AGTGAAAAGGAATGATATT
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ORGANISM: Homo sapien
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APPLICANT: Foy, Teresa M.
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Deng, Ta
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DAGMOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.42723
CURRENT APPLICATION NUMBER: US/11/344,932
CURRENT APPLICATION NUMBER: US/11/44,678
PRIOR APPLICATION NUMBER: 10/1144,678
PRIOR FILING DATE: 2001-12-01
PRIOR PELLING DATE: 2001-16-29
PRIOR PELLING DATE: 2001-16-29
PRIOR PELLING DATE: 2001-16-29
PRIOR PELLING DATE: 2001-6-29
PRIOR PELLING DATE: 2001-05-09
PRIOR PELLING DATE: 2001-01-12
PRIOR PELLING DATE: 2001-01-02
PRIOR PELLING DATE: 2000-11-02
PRIOR PELLING DATE: 2000-11-02
PRIOR PELLING DATE: 2000-11-03
PRIOR PELLING DATE: 2000-11-09
PRIOR PELLING DATE: 2000-10-09
PRI
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Search completed: December 31, 2006, 19:49:18 Job time : 561.33 secs

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GenCore version 5.1. Copyright (c) 1993 - 2006 Bioc	using sw model	Run on: December 31, 2006, 12:14:13 ; Sea (witho	Title: US-09-232-880-107 Perfect score: 1621 Sequence: 1 cgccatggcactgcagggcaa	Scoring table: IDENTITY NUC Gapop 10.0 , Gapext 1.0	Searched: 48236798 segs, 27959665780 residues	Total number of hits satisfying chosen parameters:	Minimum DB seq length: 0 Maximum DB seq length: 200000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Database : EST:* 1: gb_est1:* 2: gb_est3:* 3: gb_est4:* 4: gb_est5:* 5: gb_est6:*	7: 9b_est2:: 8: 9b_est7:* 9: 9b_est8:* 10: 9b_est9:* 11: 9b_9ss1:*	12: gb_gss2:* 13: gb_gss3:* 14: gb_gss4:*	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.	\$ Result Query No. Score Match Length DB ID	1571 96.9 1967 6 1571 96.9 3111 6	3 1532.6 94.5 1544 6 CR615811 4 1455.6 89.8 1598 6 CR618063 5 1367.8 84.4 1606 6 CR657309 6 915.2 57.7 1042 4 BX359836 7 916.4 56.5, 97.7 1 A1568928	915.6 56.5 1534 6 887.6 54.8 924 4 882.2 54.4 971 1 863 53 1081 1	848.8 52.4 955 845.8 52.2 1076 822.2 50.7 990 813.6 50.2 823	807.4 49.8 1523 6 807.4 49.8 2576 6 801 49.4 1558 6	794.4 49.0 893 1

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BX449005 BX449005
CD643323 AGENCOURT
CR856058 DKFZp469F
BQ941482 AGENCOURT
B1256256 602975075
BM675180 U1-E-EJ0-
BG289921 602381346
A1796120 DKFZp469L
BM714371 U1-E-EJ0-
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A1373640 BCZB670
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ALIGNMENTS

RESULT 1 CR625004	
LOCUS DEFINITION	CR625004 1967 bp mRNA linear HTC 21-JUL-2004 full-length cDNA clone CSODJ007Y107 of T cells (Jurkat cell line)
	Cot 10-normalized of Homo sapiens (human).
ACCESSION	CR625004
VERSION	CR625004.1 GI:50505811
KEYWORDS	HTC; CNSLT_cDNA.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
	Hominidae; Homo.
REFERENCE	1 (bases 1 to 1967)
AUTHORS	Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE	Full-length cDNA libraries and normalization
JOURNAL	Unpublished
REMARK	Contact : Feng Liang Email : fliang@lifetech.com URL :
	http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
	Faraday Avenue
REFERENCE	2 (bases 1 to 1967)
AUTHORS	Genoscope.
TITLE	Direct Submission
JOURNAL	Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
	BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
	- Web : www.genoscope.cns.fr)
COMMENT	1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
	end enriched, double-strand cDNA was digested with Not I and cloned
	into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
	was normalized. Library was constructed by Life Technologies, a
	division of Invitrogen.
FEATURES	Location/Qualifiers
source	11967
	/organism="Homo sapiens"
	/mol_type="mRNA"
	/db xref="taxon:9606"
	/tissue_type="T cells (Jurkat cell line) Cot
	10-normalized"
	/plasmid="pCMVSPORT_6"
ORIGIN	

	RESULT 2 (Ref16479 (Ref16479 (Ref16479 (Ref16479 (Ref16479 (Rull-length cDNA clone CSODKO10Y111 of HeLa cells Cot 25-normalized for Homo sapiens (human). (Ref16479 (Ref16479 (Ref16479) (Ref16479 (Ref16479) (Ref16479 (Ref16479) (Ref16479 (Ref16479) (Ref16479 (Ref16479) (Ref16479 (Ref16479) (Ref16479 (Ref16479) (Ref16479) (Ref16479 (Ref16479) (Ref16479 (Ref16479) (Ref16479 (Ref16479) (Ref16479 (Ref16479) (Ref16479 (Ref16479) (Ref16479 (Ref1647) (Ref16479 (Ref16479) (Ref16479 (Ref16479) (Ref16479 (Ref16479) (Ref16479 (Ref16479) (Ref16479 (Re
Query Match 96.94; Score 1571; DB 6; Length 1967; Best Local Similarity 99.74; Pred No. 0; Mismatches 5; Indels 0; Gaps 0; Mismatches Matches 1574; Conservative 0; Mismatches 5; Indels 0; Gaps 0; Mismatches Db 41 CGCCATGGCACTGCAGGCATCTCGGTCGTCGTCGTCGCCCCGGGCCCTT 100 CGCCATGGCACTGCAGGCATCTCGGTCGTCGTCGTCGTCGTCGCCCGGCCCGTT 100 CGCCATGGCACTGCAGGCATTCCGGGCGCTTGTGCTGGCCCCGGCCCCGGCCCCGGCCCCGGCCCCGGCCCCGGCCCC	0

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CR615811 1544 bp mRNA linear HTC 21-JUL-2004 full-length cDNA clone CS0DI027YJ12 of Placenta Cot 25-normalized of Homo sapiens (human).
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Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1544)

Li, W. B., Gruber, C., Jessee, J. and Polayes, D. Pull-length cDNA libraries and normalization

Unpublished
TTTTGAGGAGGTTGTTCATCATGATCACAACAAGAACGGGGCTCGTTTATCACCAGTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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Homo sapiens (human)
Homo sapiens
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Pred. No. 0;
0; Mismatches
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODKO10Y11"
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                                                                                                                96.9%;
larity 99.7%;
Conservative (
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Best Local Similarity
Matches 1574; Conserv
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CR618063 1598 bp mRNA linear HTC 21-JUL-2004
full-length cDNA clone CS0DM013Y103 of Fetal liver of Homo sapiens
(human).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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1 (bases 1 to 1598)

11/W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished
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CR618063.1 GI:50498870
HTC; CNSLT_CDNA.
Homo sapiens (human)
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2 (bases 1 to 1598)
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AUTHORS
TITLE
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     - Web : www.genoscope.cns.fr)

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pcMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clons="CS0D1027Y12"
/tissue_type="Placenta Cot 2'/plasmid="pCMVSPORT_6"
                                                                                                                                                                                                           Score 1532.6;
Pred. No. 0;
0; Mismatches
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Matches 1535; Conservative
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Pongo pygmaeus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Pongo.
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Genoscope.

Direct Submission

Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and Ecok withes of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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Pred. No. 8.2e-313;
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                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODMO13Y103"
/tissue_type="retal liver"
/plasmid="pcMVSPORT_6"
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/organism="Homo sapiens"
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                                                                                                               Neuharberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing
consortium of the German Genome Project.
This clone (DKFZ): Spin savailable at the RZDD Deutsches
Ressourcenzentrum fuer Genomicschung GmbH in Berlin, Germany.
Please contact RZDD for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=DKRZp46901232
Further information about the clone and the sequencing project is
available at http://mpp.gsf.de/projects/cdna/.
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    Bahr, A., Lauber, J., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and Wiemann, S. The German cDNA Consortium Direct Submission Submitted (12-NOV-2004) MIPS, Ingolstaedter Landstr. 1, D-85764
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Pred. No. 2.4e-293;
0; Mismatches 37; Indels 6;
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Contact: Genoscope
2 rue Gaston Cremiter National de Sequencage
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Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cDNA intes of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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1 (bases 1 to 977)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Pull-length cDNA libraries and normalization

Unpublished (2001)

On Feb 15, 2001 this sequence version replaced
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT & vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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25-NORMALIZED Homo sapiens CDNA
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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                                                                                                                                                                                                                                                                                                                                                                                                               Hominidae; Homo.

1 (bases 1 to 1042)

Li, W. B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization
Unpublished (2001)
On May 5, 2003 this sequence version replaced gi:30384374.
Contact: Genoscope
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Pred. No. 4.4e-197;
2; Mismatches 15;
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     CTTATATTTTGAATGGGTT 1550
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AY609940 1534 bp mRNA linear HTC 31-JAN-2005
Sus scrofa clone Clu_4587.scr.msk.pl.Contigl, mRNA sequence.
AY609940
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Hornshoj,H., Bendixen,C. and Panitz,F.
Direct Submission
Submitted (28-APR-2004) Animal Breeding and Genetics, Danish
Institute of Agricultural Sciences, Research Centre Foulum, Postbox
50, Tjele DK-8830, Denmark
                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Laurasiatheria, Cetartiodactyla, Suina, Suidae,
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Jorgensen, F.G., Hobolth, A., Hornshoj, H., Bendixen, C., Fredholm, M.
and Schierup, M.H.
Comparative analysis of protein coding sequences from human, mouse
and the domesticated pig
(er) BMC Biol. 3 (1), 2 (2005)
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264 GCCACAGGGACCGGCGGTGATGCGGCGTCTGTGCGCACTGGCGGACGTGGTGCTGAGCC
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/organism="Sus scrofa"
/mol type="mRNA"
/db_xref="taxon:9823"
/clone="Clu_4587.scr.msk.pl.Contig1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 915.6; DB 6;
Pred. No. 1.1e-192;
0; Mismatches 259;
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                                                                                                                                                              COT 10-NORMALIZED
      to sequence cluster
                                                                                                                                                  /cell_type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZEI /cell_line="T UNKAT" /clone_lib="Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
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      division of Invitrogen. This sequence belongs
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Best Local Similarity 99.4%; Pred. No. 6.6e-193;
Matches 928; Conservative 2; Mismatches 3;
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/mol_type="mRNA"
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/clone="CSODJ007Y107"
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Qy 241 CTTCGGCGGGGTGTCATGGAGAAACTCCAGCTGGGCCCAGAGATTCTGCAGCGGGAAAA 300 Db 324 CTTCGGCCTGGTGTCATGGAAAAACTCCAGCTGGGCCCAGAGACTCTACTGAGGGAGAA 383 Qy 301 TCCAAGGCTTATTATGCCAGGTGAGTGGATTTGGCCAGTCAGAAGGTTCTGCCGGTT 360 Db 384 TCCAAAGCTTATCATGCCAGGCTGAGTTGGCCAGTCAGAAAGATTCTTTCAGGT 443	Oy 361 AGCTGGCCACGATATCAACTATTTGGCTTTGTCAGGTGTTCTCTCAAAATTGGCAGAAG 420 Db 444 AGCAGGACATGACATCAACTATTTGGCTTTGTCGGGTGTTCTGTCAAGAATTGGCAGAAG 503 Oy 421 TGGTGAGAAATCCGTATGCCCGCTGAATCTCCTGGCTGACTTGCTGGTGGTGGTCTAT 480 Db 504 TGGCGAGAATCCACAAGACTCCTGGCTGACTTTGCTGGTGGCCTCAT 563	QY 481 GTGTGCACTGGCACTTATATGACGCACACGCACACGCACTGACAAGGGTCAGGT 540 DD 564 GTGTGCCCTGGGCATCATGATGGCTCTGTTTGAACGCACACGCTCTGGCAAGGGTCAGAT 623	OY 541 CATTGATGCAATATGGTGGAAGGAACAGCATATTTAAGTTCTTTTTTTGTGGAAAACTCA 600	OY 601 GAAATGGAGTCTGTGGGAAGCACCTCGAGGACAGAACATGTTGGATGGTGGAGCACCTTT 660 Db 684 ACTAACAGGACTGTGGGACCAGCTCGTGGACAGAACATGTTAGATGGTGGAGCACCTTT 743	Qy 661 CTATACGACTTACAGGACAGACAGGGGAATTCATGGCTGTTGGAGCAATAGAACCCCA 720 Db 744 CTACACGACCTACAAGACGGCCGACGGGGTTCATGGCTGTTGGAGCAATCGAGCAGAA 803	QY 721 GTTCTACGAGGGGTGCTGGACTAGAGGTCTGGTGAACTTCCCCAATCAGT 780 D 1	OY 781 GAGCATGGATGATTGGAGAAATGAAGAAGATTTGCAGATGTATTTGCAAAGAAGAC 840 DD 864 GAGCATAAGGGATTGGCCAGAAATGAAGAAATTTGCAGATGTATTTGCAAAGAAGAC 923	OY 841 GAAGGCAGAGTGTCAAATCTTTGACGCACAGATGCCTGTGTGACTCCGGTTCTGAC 900	Qy 901 TTTGAGGAGGTTGTTCATCATGATCACAAGGAACGGGGCTCGTTTATCACCAGTGA 960 Db 984 TCTGGAAGAGGTTGCGCATCATGGTCATAACAAAGATCGGGGCTCATTTATTACTGACGG 1043	Oy 961 GGAGGAGGACGTGAGCCCCCGCCCTCTGCTGTTAAACACCCCCAGCCATCCCTTC 1020 Db 1044 GGAGCAGGGTGTGAGTCCCCGCCCTGCACCTCTTCTCTCCAACACCCCAGCCGTCCCATC 1103	OY 1021 TTTCAAAAGGGATCCTTTCATAGGAGAACACACTGAGGAGATACTTGAAGAATTTGGATT 1080	Oy 1081 CAGCCGCGAAGAGATTTATCAGCTTAACTCAGATAAAATCATTGAAAGTAATAAAGGTAAA 1140	AGCTAGTCTCTAACTTCCAGGCCCACGGCTCAAGTGAATTTGAATACTGCAT	1193 TTACAGTGTAGAGTAACACA-TAACATTGTATGGATGGAAACATGGAGGAACAGTATTAC	Db 1284 TTÁCÁGTATÁGTGTÁÁTGCÁGAÁAATCGTATGCÁTAGÁÁAGAGAGAAÁCAATÁTCAC 1343 Oy 1252 AGTGTCCTACCACTCTAATCAAGAAAGAATTACAGACTCTGATTCTACAGTGATGATTG 1311	Db 1344 AGTGGTCCAGCTATTCTAATCAGGAACAAGATTCTGCTTATACAGTAATGATCG 1398 Qy 1312 AATTCTAAAAATGGTTATCATTAGGCTTTTGATTTATAAAACTTTGGGTACTTATACTA 1371

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end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
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                                                                                                                                                                                                                                                  /Lissue type="PLACENTA COT 25-NORMALIZED"
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/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR v
sites of the pCMVSPORT 6 vector. Library was normalized.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AACTTCCAGGCCCACGGCTCAAGTGAATTTGAATACTGCATTTACAGTGTAGAGTAACAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACAGAACAGMAGATGGGGAATTCATGGCTGTTGGAGCAATAGAACCCCAGTTCTACGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGCTGATCAAAGGACTTGGACTAAAGTCTGATGAACTTCCCAATCAGATGAGCATGGATG
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                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 54.4%; Score 882.2; DB 1; Best Local Similarity 96.3%; Pred. No. 2.7e-185; Matches 893; Conservative 10; Mismatches 23;
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/clone="CS0D1027YJ12"
                                                                                                                                    Location/Qualifiers
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National
Z rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Ist strand cDNA was primed with a NotI-oligo(dT) primer. Five I
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1 (bases 1 to 971)

Li, W.B. , Gruber, C., Jessee, J. and Polayes, D.

Unpublished (2001)
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/db xref="taxon.9606"
/db xref="taxon.9606"
/clone="IMAGE:4776971"
/lab host="H10B (Ti phage-resistant)"
/clone_lib="NCI CGAP_Skn3"
/note="Organ: skin, Vector: pcMV-SPORT6; Site_1: NotI;
/incte="Csall; Cloned unidirectionally. Primer: Oligo dT
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Technologies. Note: this is a NCI_CGAP Library."
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                                                                               Email: cgapD8-r@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Flate: LLAMIGSO row: f column: 12
High quality sequence stop: 805.
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Pred. No. 7.3e-178;
0; Mismatches 37;
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                                                                     Contact: Robert Strausberg, Ph.D.
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Best Local Similarity 95.7%;
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ALSS5978 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens CDNA clone CSODK010X111 5-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                   993 IGCIGITAAACACCCCAGCCAICCCIICITICAAAAGGGAICCTITCAIAGGAACACA 1052
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                                                                                        GTTTGCAGATGTATTTGCAAAGAAGACGAAGAGTGGTGTGTCAAATCTTTGACGGCAC 720
                                                                                                                              874 AGATGCCTGTGTGACTCCGGTTCTGACTTTTGAGGAGGTTGTTCATCATGATCACAAA 933
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/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer: Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
839 GGTTGTTABAACACCCCAGACATCCCTTCTTCAAACGGGATCCTTTCATAGGAGAACACC
                                                                                                                                                                                                                                 For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CS0DK010AE06QP1&c=2801.r. Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSOBKO10Y111"
/cell_type="HELA CELLS COT 25-NORMALIZED"
/cell_line="HELA"
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VERSION AL551698.3 GI:45856497 KEYWORDS SOURCE Home sapiens CRGANISM Home sapiens Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Home 990) AUTHORS Li, M. B., Gruber, C., Jessee, J. and Polayes, D. TITLE Full-length CDNA libraries and normalization JOURNAL COMMENT On Peb 15, 2001 this sequence version replaced gi:31273514.	Conteact: Genoscope Genoscope - Centre National de Sequencage Genoscope - Centre National de Sequencage 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE Emal: seqrefégenoscope.cns.fr, Web: www.genoscope.cns.fr 1st strand cDNA was primed with a NotI-oligo(dI) primer. Five prime end enrichted, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster	FOR more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODIO62CH03QPl&c=2801.r. Location/Qualifiers 1990 990 /	Query Match Query Match Query Match Query Match Matches 855; Conservative 11; Mismatches 31; Indels 2; Gaps 2;	Qy 1 CGCCATGGCACTGCAGGCATCTCGGTCATGGAGCTGTCCGGCCCGGGCCCGTT 60	Qy 121 CCGCTACGACGTCAGGCCGCTTGGGCCAGGCAAGCGCTAGTGCTGGACCTGAAGCA 180 Db 133 CCGCTACGACGCCGTTGGGCCGGGGCAGCGCTCGCTTGGTCGTGAAGCA 192 Qy 181 GCGGGGGGGGCGCGTGCTGCGGCTCTGTGTGCTGGATGTGCTGGAGGC 240	Db 193 GCCGCGGGGGGCCGTGCTGCTGTACAAGCSGTCSGATGTGCTGCTGCTGGAGCC 252 Qy 241 CTTCCGCCGGGGTGTCATGGAGAAACTCCAGCTGGGCCCAGAGATTCTGCAGCGGGAAAA 300	Qy 301 TCCAAGGCTTATTATGCCAGGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCCGGTT 360	Qy 36.1 AGCTGGCCACGATATCAACTATTTGGCTTTGTCAGGTGTTCTCTCAAAAATTGGCAGAAG 420 11
CGCCATGCAGGCATCTCGGTCATGAGGCTGTCCGGCCTGGCCCGGGCCCGTT	193 CCGCTACGACGTGAGCCGGGGGCAAGCGCTCGCTAGTGCTGGAGCGCTGGAAGCA 181 GCCGCGGGGAAGCCGCGTGCGCGCGTCTGTGCAAGCGCTCGATGCTGCTGCTGGAGCA 253 GCCGCGGGGAGCCGCCGTGCTGCGGCGTCTGTGCAAGCGGTCGGATGTGCTGCTGGAGCC 241 CTTCCGCCGCGGTGTCATGGAGAAACTCCAGCTGGGCCCAGAGATTCTGCAGCGGAAA 313 CTTCCGCCGGGGTGTCATGGAAAACTCCAGCTGGGCCCAGAGATTCTGCAGCGGGAAA 314 CTTCCGCCGGGGTGTCATGGAAAACTCCAGCTGGGCCCAGAGATTCTGCAGCGGGAAA 315 CTTCCGCCGGGGTGTCATGGAAAACTCCAGCTGGGGCCCAGAGATTCTGCAGCGGGAAA 316 CTTCCGCCGGGGTGTCATGGGAAAACTCCAGCTGGGGGCCCCAGAGATTCTGCAGCGGGAAAA CTTCCGCCGGGGTGTCATGGGAAAACTCCAGCTGGGGGGCCCCAGAAATTCTGCAGCGGGGAAAA CTTCCGCCGGGGTGTCATGGGAAAACTCCAGCTGGGGGGCCCCAGAAATTCTGCAGCGGGGAAAA CTTCCACACACACACACACACACACACACACACA	1	Qy 481 GTGTGCACTGGGCAT-TATAATGGCTCTTTTTGACCGCACGCACGACGACGGGTCAGG 539 Db 553 GTGTGCACTGGCATATATAATGGCTCTTTTTTGACCGCACAGGCACGGCAAGGGTCAGG 612 Qy 540 TCATTGATGCAAATATGGTGGAAGGAACAGCATATTTAAGTTCTTTTCTGTGGAAAACTC 599 Db 613 TCATTGATGCAAATATGGTGGAAGGAACAGCATATTTAAGTTCTTTTCTGTGGAAAACTC 672	Qy 600 AGAAATCGAGTAAGCACCTCGAGGACAGAACATGTTGGATGGTGGAGCACCTT 659 Db	Qy 720 AGTICTACGAGCTGCTGALCAAAGGACTTGGACTAGAGTCTGAACTTCCCAATCAGA 779 Db	Db 853 TGAGCATGATGATGASCAGAAATGAAGAAGAARTTTGCAGATGTATTTGSAAARAAAA 912 Qy 840 CGAAGGCAGAGTGGTCAAATCTTTGACGGCACAGATGCCTGTGTGACTCCGGTTCTGA 899 : - -	Qy 900 CTTTGAGGAGGTTGTTCATCATGA 924 Db 970 TTTTGAGGAGKTGTTCTCATAATAA 994	RESULT 14 AL551698 LOCUS AL551698 DEFINITION AL551698 PLACENTA COT 25-NORMALIZED Homo sapiens PLACENTA Sequence.

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AL551698 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA CLORD CLORD CSUDIO62YP05 5-PRIME, mRNA sequence.

ACCESSION

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50.2%;
99.1%;
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Best Local Similarity 99.1<sup>1</sup>
Matches 816; Conservative
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Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa Clone Distribution: Researchers may obtain clones from Research Seq primer: M13 Reverse.
                                                                                                    GAAATCGAGTCTGTGGGAAGCACCTCGAGGACAGAACATGTTGGATGGTGGAGCACCTTT 660
                                                                                                                  CTATACGACTTACAGGACAGCAGATGGGGAATTCATGGCTGTTGGAGCAATAGAACCCCA 720
                                                                                                                                                                               CTATACGACTTACAGGACAGACAGATGGGGAATTCATGGCTGTTGGAGCAATAGAACCCCA 732
                                                                                                                                                                                                                          GTTCTACGAGCTGCTGATCAAAGGACTTGGACTAAAGTCTGATGAACTTCCCAATCAGAT 780
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GTGTGCACTGGGCATTATAAATGGCTCTTTTTGACCGCACAGGACTGACAAGGGTCAAGT 552
                                                                      CATTNATGCAAATATNGTGGAAGGAACAGCATATTTAAGTTCTTTTGTGTGGAAAACTCA 612
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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optic nerve, retina, Retina Foveal and Macular, RPE and
Choroid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to facilitate gene
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UI-E-EJO-aiq-n-09-0-UI.rl UI-E-EJO Homo sapiens CDNA clone
UI-E-EJO-aiq-n-09-0-UI 5', mRNA sequence.
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Coordinated Laboratory for Computational Genomics
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1 (bases 1 to 823)

10 (bases 1 to 823)

Normalization and subtraction: two approaches
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BM723657.1 GI:19044988
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Homo sapiens
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AUTHORS
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/lab host="DH10B (Life Technologies) (T1 phage resistant)"
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GGTAC	=	GTAC
CTTTG	<u>=</u>	CTTTC
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PN JP 2001513886-A/107
PN JP 200151386-A/107
PN JERE-1998 JP 1998537008
PR 25-FEB-1999 JD 08/806596,01-AUG-1997 US 08/904809 PR 09-FEB-1999 US 09/020747
PI JIANGCHUN XU, DAVIN C DILLON
PC G01N33/574,G01N33/577,C07KL6/30,A61K39/395,A61K47/48,C12Q1/68,PC G01N33/543
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CC Topology: Linear;
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1 (bases 1 to 1621)
Xu,J and Dillon, D. C.
Compounds for immunodiagnosis of prostate cancer and methods for
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25-FEB-1998 JP 1998537008
25-FEB-1997 US 08/806596
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JP 2001513886-A/107.
Homo sapiens (human)
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GITCTACGAGCTGCTGATCAAAGGACTTGGACTAAAGTCTGATGAACTTCCCAATCAGAT
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C12N5/10,
C12P21/08,C12Q1/68,G01N33/574,G01N33/68//A61P35/00,C12N15/00,
A61K37/02,
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/organism='Homo sapiens (human)'.
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/ .Cycanism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Lis,Xx., Wang,A., Skelky,Y.A.W.,
Hepler,W.T. and Henderson,R.A.

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Xu,J., Dillon,D.C. and Mitcham,J.L.
Compounds for immunotherapy of prostate
their use
Patent: US 6465611-A 107 15-OCT-2002;
Corixa Corporation; Seattle, WA
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/organism="unknown"
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Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Yuqiu,J.,
Reed,S.G., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A. and
                                                                     961 GGAGGAGGAGGTGGGGCCCCGCCCTGCACCTGCTGTTAAACACCCCCAGCCATCCCTTC
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Patent: US 6129505-A 107 11-DEC-2001;
Corixa Corporation; Seattle, WA
Location/Qualifiers
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Patent: US 6512094-A 107 28-JAN-2003;
Corixa Corporation; Seattle, WA
Location/Qualifiers
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llarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches

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/organism="unknown"
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Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L.
Prostate specific fusion protein compositions
Patent: US 6395278-A 107 28-MAY-2002;
Corixa Corporation; Seattle, WA
Location/Qualifiers
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Matches 1621; Conservative 0; Mismatches

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	RESULT 11 AR563606 LOCUS DEPUNTION Sequence 107 from patent US 6759515. ACCESSION AR563606 VERSION AR563606. KEYWORDS SOURCE Unknown. ORGANISM Unknown.	REFERENCE 1 (bases 1 to 1621) AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H., Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skelky,Y.A.W., Hepler,W.T. and Henderson,R.A. TITLE Compositions and methods for the therapy and diagnosis of prostate cancer: US 6759515-A 107 06-JUL-2004; Corixa Corporation; Seattle, WA PEATURES Location/Qualifiers SOURCE	tch al Similari 1621; Cons 1 CGCCATG	CTGTGCTATGGTCCTGGCTGCTTGGGCGCGCGTGGTAGGTA	Qy 181 GCCGCGGGGAGCCGCCGTGCTGCGGCGTCTGTGCAGCGGTCGGAGTCTGCTGCTGCTGCGAGCC 240 Db 181 GCCGCGGGGAGCCGCGTGCTGCGGCGTCTGCAGCGGTCGGATCTGCTGCTGGAGCC 240 Qy 241 CTTCCGCCGCGGTGTCATGAGAAACTCCAGCTGGGCCCAGAGATTCTGCAGCGGAAAA 300 Db 241 CTTCCGCCGCGGTGTCATGGAGAAACTCCAGCTGGGGCCCAGAGATTCTGCAGCGGGAAAA 300 Qy 301 TCCAAGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCCGGTT 360 Db 301 TCCAAGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCCGGTT 360 Bb 301 TCCAAGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCCGGTT 360
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SUMMARIES

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	Score	1621	1621	1621	1621	1621	1621	1621	1621	1621	1621	1621	1621	1621	1621	1621	1621	1621	1621	515	515	515	515	515
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	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	US-09-159-812-74	US-03-636-ZIS-/4	US-09-685-166A-74	US-09-115-453-74	US-09-688-489-74	US-09-679-426-74	US-09-759-143-74	US-09-651-236-74	US-09-030-606-74	US-09-657-279-74	US-10-012-896-74	US-09-116-134-74	US-10-144-678A-74	US-09-702-705-1504	US-09-736-457-1504	US-09-614-124B-1504	US-09-671-325-1504	US-09-658-824-1504	US-10-017-754-1504	US-09-651-563-1504	US-09-020-956-3	US-09-030-607-3
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ALIGNMENTS

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GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
C. TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
NUMBER OF SEQUENCES: 178
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1621;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/020,956
FILING DATE: 09-FEB-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 3;
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100.0%; Score 1621;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1621; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 210121.427C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                           Sequence 107, Application US/09020956 Patent No. 6261562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
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RESULT 1
US-09-020-956-107
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APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Harlocker, Susan Louise
APPLICANT: Harlocker, Susan Louise
APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Retter, Mark
APPLICANT: Retter, Mark
APPLICANT: Solk, John
APPLICANT: DIAGNOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DAGNOSIS OF PROSTATE CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 107, Application US/09439313
Patent No. 6329505
GENERAL INFORMATION:
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Pred. No. 0;
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INFORMATION FOR SEQ ID NO: 107
SEQUENCE CHARACTERISTICS:
LENGTH: 1621 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
                                                                                                                                    ; ORGANISM: Homo sapiens
US-09-030-607-107
                                                                                                                                                                                   Query Match 100.
Best Local Similarity 100.
Matches 1621; Conservative
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; Sequence 107, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Mitcham, Jennifer Lynn
; APPLICANT: Witcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION UNDMER: US/09/352,616A
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFFWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 107
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larity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
  FILE REFERENCE: 210121.427C9
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: EastSEQ for Windows Version 3.0
SEQ ID NO 107
LENGTH: 1621
                                                                                                                                                      TYPE: DNA
CORGANISM: Homo sapien
US-09-439-313-107
                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 1621; Conserv
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; Sequence 107, Application US/09232149A
; Patent No. 6465611
; GRERRAL INFORMATION:
    APPLICANT: Xu, Jiangchun
; APPLICANT: Mi, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TILLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; TILLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
; TILLE REFERENCE: 210121.427C6
; CURRENT APPLICATION NUMBER: US/09/232,149A
; CURRENT FILLING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1077
LENGTH: 1621
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	RESULT 7 US-09-636-215-107 is Sequence 107, Application US/09636215 is Patent No. 6620922 is GENERAL INFORMATION: is APPLICANT: Witcham, Jennifer L. is APPLICANT: Mitcham, Jennifer L. is APPLICANT: Mitcham, Jennifer L. is APPLICANT: Harlocker, Susan L. is APPLICANT: Henderson, Robert A. is APPLICANT: Henderson, Robert A. is APPLICANT: Retter, Marc W. is APPLICANT: Retter, Marc W. is APPLICANT: Retter, Marc W. is APPLICANT: Retter, Marc W. is APPLICANT: Cariof H. is APPLICANT: Cariof H. is APPLICANT: Cariof H. is APPLICANT: Cariof H. is APPLICANT: Cariof H. is APPLICANT: Cariof H. is APPLICANT: Cariof H. is APPLICANT: Cariof H. is APPLICANT: Cariof H. is APPLICANT: Cariof H. is APPLICANT: Cariof H. is APPLICANT: Cariof H. is APPLICANT: Cariof H. is APPLICANT: Li. Samuel	o this galages	US-09-636-215-107 Query Match
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141 AGCTAGTCTCTAACTTCCAGGCCCAGGGTGAATTTGAATACTGCATTTACAGTG 120	RESULT 8 US-09-685-16A-107 Sequence 107, Application US/09685166A Patent No. 6630305 GENERAL INPORMATION: APPLICANT: Xu, Jiangchun APPLICANT: Dillon, Davin C. APPLICANT: Harlocker, Susan L. APPLICANT: Harlocker, Susan L. APPLICANT: Handerson, Robert A. APPLICANT: Handerson, Robert A. APPLICANT: Handerson, Robert A. APPLICANT: Retter, Marc W. APPLICANT: Retter, Marc W. APPLICANT: Retter, Marc W. APPLICANT: Bay, Craig H. APPLICANT: Day, Craig H. APPLICANT: Day, Craig H. APPLICANT: Carter, Darrick APPLICANT: Skeiky, Yasir A.W. APPLICANT: Skeiky, Yasir A.W. APPLICANT: Skeiky, Yasir A.W. APPLICANT: Skeiky, Wasir A.W. APPLICANT: Skeiky, Wasir A.W. APPLICANT: Skeiky, 13011am TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER TITLE OF INVENTION: US/09/685,166A CURRENT FILID APPLICATION NUMBER: US/09/685,166A CURRENT FILID APPLICANTON NUMBER: 2000-10-10 NUMBER OF SEQ ID NOS: 998 SOFTWARE: PastSEQ for Windows Version 3.0 SEQ ID NO 107 TTENDER: DNA TYPER: DN
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61 CTGCTACGCCTCGCCTCGGGCCCTGTGGTACCCGTGGCCCGGCCCCCCCC	601 GAAATCGAGTCTGGGAAGCACCTCGAGGACAGAACATGTTGGATGGTGGAGCACCTTT 660 601 GAAATCGAGTCTGGGGAAGCACCTCGAGGACAGAACATGTTGGATGGTGGAGCACCTTT 660 601 GAAATCGGACTTACAGGACAGCAGAGGACAGAACATGTTGGATGGTGGAGCACCTTT 660 601 CTATACGACTTACAGGACAGCAGATGGGGAATTCATGGCTGTTGGAGCAATAGAACCCCA 720 721 GTTCTACGAGCTTGCACAGATGGGGAATTCATGGCTGTTGGAGCAATAGAACCCCA 720 721 GTTCTACGAGCTGCTGATCAAAGGACTTGGACTTTGGAGCAATAGAACCCCA 720 721 GTTCTACGAGCTGCTGATCAAAGGACTTGGACTAAAGTCTGATGAACTACAATAGAACCCCA 720 721 GTTCTACGAGCTGCTGATCAAAGGACTTGGACTAAAGTCTCATGAACAAGAAC 840 841 GAAGCAGGATGATTGACGAGAATGAAGAACTTGCCAATCAAACAACAAGAACAACAAAAGAAATGAAATGAAAAGAACAAAATGAAAAGAAATGAAAAGAAATGAAAAGAAATGAAAAGAAATGAAAAGAAATGAAAAAGAAATGAAAACAAAACAAAACAAAACAAAC

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1. COCCUP.COM.CONTROCTOR.CONTROCT			1321 AATGGTTATCATTAGGGCTTTTGATTTATAAACTTTGGGTACTTATACTAAATTATGGT 	1381 AGTTATTCTGCCTTCCAGTTTGCTTCATATATTGTTGATATTAAGATTCTTGACTTATA 1381 AGTTATTCTGCCTTCCAGTTTGCTTGATTTTGTTGATATTAAGATTCTTGACTTATA AMAGTTATTCTGCCTTCCAGTTTGCTTGATTTTGTTGATATTAAGATTCTTGACTTATATA AMAGTTATTCTGCTTTGCTTGCTTGATATTTTGTTGATATTAAGATTCTTGACTTATATA	1441 TTTTGAATGGGTTCTAGTGAAAAGGAATGATATTCTTGAAGACATCGATATTTTTTTT		1561 AAAAGCACGIGAAACAAAAAAAAAAAAAAAAAAAAAAAA	UY 1621 A 1621 Db 1621 A 1621	NS-09-651-236-107 Sequence 107, Application US/09651236	GENERAL INFORMATION: ; APPLICANT: Xu, Jiangchun ; APPLICANT: Dillon, Davin C.	Harlocker, Susan I Jiang, Yuqui Henderson, Robert	APPLICANT: Retter, Marc W. ; APPLICANT: Retter, Marc W. ; APPLICANT: Stolk, John A. ; APPLICANT: Stolk, John A.		APPLICANT: Walliam A.W. APPLICANT: Skeiky, Yaair A.W. APPLICANT: Hepler, William BETHODS FOR THE THERAPY AND THILE OF INVENTION: OPPOSETIONS AND METHODS FOR THE THERAPY AND THILE OF INVENTION: OPPOSEMENTE OF TANGED	1142718C18 NUMBER: US/09/651,236	S.	; TYPE: DNA ; ORGANISM: Homo Bapien US-09-651-236-107
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Patent No. 6894146
Patent No. 6894146
PAPLICANT: Xu, Jiangchun APPLICANT: Xu, Jiangchun APPLICANT: Dillon, Davin C. APPLICANT: Mitcham, Jennifer L. APPLICANT: Harlocker, Susan L.
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Henderson, Robert A
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
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REFERENCE/DOCKET NUMBER: 210121.428C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 107:
SEQUENCE CHARACTERISTICS:
LENGTH: 1621 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECTLE TYPE: CDNA
ORIGINAL SOURCE:
                                                                                                                                                                                                         100.0%; Score 1621;
100.0%; Pred. No. 0;
ive 0; Mismatches
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Matches 1621; Conservative
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APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedyick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Li, Samuel
APPLICANT: Li, Samuel
APPLICANT: Wang, Aljun
APPLICANT: Hepler, William
TITLE OF INVENTION: DIAGNOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C19
CURRENT PILING DATE: 2000-09-06
NUMBER OF SEQ ID NOS: 877
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 107
LENGTH: 1621
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1621; Conservative 0; Mismatches
                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapien
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1440 1080 1140 1320 1320 1380 1500 TTTCAAAAGGGATCCTTTCATAGGAGAACACTGAGGAGATACTTGAAGAATTTGGATT 1080 900 TITIGAGGAGGITGITCATCATGATCACAACAAGGAACGGGGCTCGTTTATCACCAGTGA 960 780 AGTTATTCTGCCTTCCAGTTTGCTTGATATTTGTTGATATTAAGATTCTTGACTTATA TTTTGAATGGGTTCTAGTGAAAAAGGAATGATATATTTTTTGAAGACATCGATATACATTT GAAGGCAGAGTGTGTCAAATCTTTGACGGCACAGATGCCTGTGTGACTCCGGTTCTGAC 1141 AGCTAGTCTCTAACTTCCAGGCCCACGGCTCAAGTGAATTTGAATACTGCATTTACAGTG CCACTCTAATCAAGAAAAGAATTACAGACTCTGATTCTACAGTGATGATTCTAAA

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1: FEMC_Celerra_SIDSJ/ptodata/2/pubpna/USO7_PUBCOMB.seq:*

2: FEMC_Celerra_SIDSJ/ptodata/2/pubpna/USO8_PUBCOMB.seq:*

3: FEMC_Celerra_SIDSJ/ptodata/2/pubpna/USO8_PUBCOMB.seq:*

3: FEMC_Celerra_SIDSJ/ptodata/2/pubpna/USO9_PUBCOMB.seq:*

5: FEMC_Celerra_SIDSJ/ptodata/2/pubpna/USO9_PUBCOMB.seq:*

5: FEMC_Celerra_SIDSJ/ptodata/2/pubpna/USO0_PUBCOMB.seq:*

6: FEMC_Celerra_SIDSJ/ptodata/2/pubpna/USO0_PUBCOMB.seq:*

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8: FEMC_Celerra_SIDSJ/ptodata/2/pubpna/USO0_PUBCOMB.seq:*

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14: FEMC_Celerra_SIDSJ/ptodata/2/pubpna/USO0_PUBCOMB.seq:*

15: FEMC_Celerra_SIDSJ/ptodata/2/pubpna/USO0_PUBCOMB.seq:*

16: FEMC_Celerra_SIDSJ/ptodata/2/pubpna/USO0_PUBCOMB.seq:*

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16: FEMC_Celerra_SIDSJ/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description	Sequence	Sequence	Sequence	Sequen	Sequenc	Sequenc	Seguenc										
SUMMERTES	O1	US-09-759-143-107	US-09-780-669-107	US-09-030-606-107	US-09-822-827-107	US-09-115-453-107	US-09-232-880-107	US-09-895-793-107	US-09-895-814-107	US-10-012-896-107	US-10-010-940-107	US-10-144-678A-107	US-10-294-025-107	US-10-688-838-107	US-11-234-786-107	US-10-357-930-21284	US-10-357-930-21872	US-10-357-930-25228
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18	1577.4	97.3	2376	σ	US-10-357-930-27126	Sequence 27126, A
19	1575.8	97.2	2069	ø	US-10-205-823-25	Sequence 25, Appl
20	1575.8	97.2	2069	13	US-11-051-454-25	Sequence 25, Appl
21	1574.2	97.1	2005	m	US-09-967-305-1	Seguence 1, Appli
22	1574.2	97.1	2005	m	US-09-967-305-10	Sequence 10, Appl
23	1574.2	97.1	2005	7	US-10-210-120-104	Sequence 104, App
24	1574.2	97.1	2002	10	US-10-909-035-104	Sequence 104, App
25	1574.2	97.1	2069	m	US-09-967-305-4	Sequence 4, Appli
26	1574.2	97.1	2069	9	US-10-205-823-17	Sequence 17, Appl
27	1574.2	97.1	2069	13	US-11-051-454-17	Sequence 17, Appl
28	1574.2	97.1	3184	16	US-11-203-526-3	Sequence 3, Appli
29	1524.8	94.1	2068	7	US-10-295-027-1134	Sequence 1134, Ap
30	1524.8	94.1	2068	œ	US-10-316-540-11	Sequence 11, Appl
31	1524.8	94.1	2068	10	US-10-756-149-1746	Sequence 1746, Ap
32	1245.4	76.8	2946	9	US-10-205-823-29	Sequence 29, Appl
33	1245.4	76.8	2946	œ	US-10-316-540-13	Sequence 13, Appl
34	1245.4	76.8	2946	13	US-11-051-454-29	Sequence 29, Appl
35	1243.8	76.7	3023	ო	US-09-967-305-8	Sequence 8, Appli
36	1243.8	76.7	3023	9	US-10-205-823-21	Sequence 21, Appl
37	1243.8	76.7	3023	13	US-11-051-454-21	Sequence 21, Appl
38	1142.8	70.5	1146	ო	US-09-967-305-3	Sequence 3, Appli
39	1134.4	70.0	2626	9	US-10-205-823-27	Sequence 27, Appl
40	1134.4	70.0	2626	13	US-11-051-454-27	Sequence 27, Appl
41	1132.8	69.9	3654	٣	US-09-967-305-6	Sequence 6, Appli
42	1132.8	6.69	3654	9	US-10-205-823-19	Sequence 19, Appl
43	1132.8	69.6	3654	13	US-11-051-454-19	Sequence 19, Appl
44	1132.8	6.69	3654	16	US-11-203-526-5	Sequence 5, Appli
45	940	58.0	1039	80	US-10-378-029-3	Sequence 3, Appli

ALIGNMENTS

Gaps APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C23 ö Length 1621; Indels 0; DB 3; Query Match
100.0%; Score 1621;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1621; Conservative 0; Mismatches CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: PASKEEQ for Windows Version 3.0 Sequence 107, Application US/09759143 Patent No. US20020022248A1 Xu, Jiangchun Dillon, Davin C. Mitcham, Jennifer L. Jiang, Yuqui Henderson, Robert A. Kalos, Michael D. Harlocker, Susan L. Ś Day, Craig H. Vedvick, Thomas S Carter, Darrick Fanger, Gary R. Retter, Marc W. Stolk, John A. Wang, Aijun Li, Samuel INFORMATION TYPE: DNA
CRGANISM: HOMC
US-09-759-143-107 SEQ ID NO 107 APPLICANT:
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1 CGCCATGGCACTGCAGGCCATCTCGGTCATGGAGCTGTCCGGCCTGGCCCCGGGCCCGGTT 60

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3 6 8	1 CECCATGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	Oy 1141 AGCTAGTCTCTAACTTCC/ 	AGCTAGICICTAACITCCAGGCCCACGCTCAAGIGAAITTGAAIACIGCAITTACAGIG 1200
8 8	CGCTACGACGTGACCTGAGGCGGAAGGGCTCGGTAGTGCTGAACCTGAAGGCTCGCTAGTGCTGGACGTGAAGGCTTGGTAGTGCTGAAGCGTTGGTAGTGCTGAAGGCTTGAGGCTAGTAGTGCTGAAGGCTTAGTAGTGCTGAAGCGTAGTAGTGCTTGAAGGCTAAGAGCTAAGTGCTTGAACCTGAAGGCTAAGTGCTTGAACCTGAAGGCTAAGTGCTTGAACCTTGAAGCTAAGAGCTAAGTGCTTGAACCTGAAGGCTAAGTGCTTGAACCTTGAAGCTAAGAGCTAAGTGCTTGAACCTTGAAGCTAAGAAGCTAAGTGCTTGAACCTTGAAGCTAAGAACTTGAAGTGCTTGAAGCTAAGAACTTGAAGTGCTTAGAACCTTGAAGCTAAAAGTAGTTGAACTTGAAGCTAAAAGTAAGT	Oy 1201 TAGAGTAACACATAACAT:	TAGAGTAACACATAÁATTGTATGCATGGAAACATGGAGGAACAGTATTACAGTGTCCTA 1260
<i>∂</i> €	GCGGCGGGGAGACCGCCGTGCTGCGGCGTCTGTGCAAGCGGTCGGATGTGCTGCTGGAGCC 2	Qy 1261 CCACTCTAATCAAGAAAAC	CCACTCTAATCAAGAAAAGAATTACAGACTCTGATTCTACAGTGATGATTGAATTCTAAA 1320
8 & 8	CTTCCGCCGCGCTGTCATGGAGAAACTCCAGCTGGGCCCAGAGATTCTGCAGCGGCAAAA [Qy 1321 AATGGTTATCATTAGGGC: 	aatggttatcattagggcttttgatttataaaactttgggtacttatactaaattatggt 1380
& 8		Qy 1381 AGTTATTCTGCCTTCCAG: 	AGTIATICTGCCTTCCAGTITGCTTGATATATGTTGATATTAAGATTCTTGACTTATA 1440
<i>&</i> 8	4 4	Qy 1441 TTTTGAATGGGTTCTAGTC	TTTTGAATGGGTTCTAGTGAAAAGGAATGATATATTCTTGAAGACATGGATATACATTT 1500
<i>&</i> 8	21 TGGTGAGAATCCGTATGCCCCGGTGAATCTCCTGGCTGACTTTGCTGGTGGTGGCCTTAT 	Qy 1501 ATTTACACTCTTGATTCT)	atttacactcttgattctacaatgtagaaaatgaggaaatgccacaaattgtatggtgat 1560
<i>≿</i> 8	GTGTGCACTGGGCATTATAATGGCTCTTTTTGACCGCACGCA	Oy 1561 AAANGTCACGTGAAACAAN 	aaangtcacgtgaaacaaaaaaaaaaaaaaaaaaaaaaaa
& a	41 CATTGATGCAAATATGGTGGAAGGAACAGCATATTTAAGTTCTTTTCTGTGGAAAACTCA 	Oy 1621 A 1621 Db 1621 A 1621	
& €.	601 GAAATCGAGTCTGTGGGAAGCACCTCGAGGACAGAACATGTTGGATGGTGGAGCACCTTT 660 	ш ол	9090806
දු පු	661 CTATACGACTTACAGGACAGAGAGGGGAATTCATGGCTGTTGGAGCAATAGAACCCCA 720 	GENERAL INFORMATION: APPLICANT: Xu, Jiang	
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& 8 &	901 TTTTGAGGAGGTTGTTCATCATGATCACAAGGAACGGGGCTCGTTTATCACCAGTGA 960) OPERATING SYSTEM: PC-DOS/MS-DOS) SOFTWARE: Patentin Release #1.0,) CURRENT APPLICATION DATA:) APPLICATION NUMBER: US/09/030,60 FILING DATE: 25-FEB-1998) CLASSIFICATION:	bos/ms-bos Aelease #1.0, Version #1.30 Ra: US/09/030,606 -1998

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GAGCATGGATGATTGGCCCAGAAATGAAGAAGAAGAAGTTTGCAGATGTATTTGCAAAGAAGAAGAC
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Fatent No. US20020081680A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR T
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.534C1
CURRENT APPLICATION NUMBER: US/09/822,827
CURRENT FILING DATE: 2001-03-28
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ATTORNEY/AGENT INFORMATION:
NAMME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.428C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-6931
INFORMATION FOR SEQ ID NO: 107:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                     Score 1621;
Pred. No. 0;
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                                                                                                                  LENGTH: 1621 base pairs
TYPE: nucleic acid
STRANDENNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
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Matches 1621; Conser
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US-09-030-606-107
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Patent No. US20020090372A1
GENERAL INFORMATION:
APPLICANT: Xu, Janagchun
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF
TITLE OF INVENTION: MATHODS FOR THEIR USE
TITLE OF INVENTION NETHODS FOR THEIR USE
TITLE OF UNENTION: COMPOUNDS FOR THEIR USE
CURRENT APPLICATION NUMBER: US/09/115,453B
CURRENT FILING DATE: 1998-07-14
NUMBER OF SEQ ID NOS: 228
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 107
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NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 107
LENGTH: 1621
                                                                                                           Query Match
Best Local Similarity 100.0%;
Matches 1621; Conservative 0;
                                                     ; TYPE: DNA
; ORGANISM: Homo sapien
US-09-822-827-107
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Best Local Similarity 100.0%; Pred. No. 0; Indels 0; Gaps 0; Matches 1621; Conservative 0; Mismatches 0; Indels 0; Gaps 0; CGCATGGCAGGCATCTCGGTCATGGAGGTGTCCGGCCCGTGCCGGGCCGTT 0	CCGCTACGAGGCCGCTTGGGCCGGGGCTAGGCCTCGCTAGTGCTGGACCTGGAGGCAGCCTAGGCGCTGGAGCACTGGGCCGGGGGCTTGGTAGTGCTGGTGCTGGAGCACTGGGCGCGGGGGGGCTTGGTGCAAGCGCTGGTGGAGCGCTGGAGCGCCGGGGGGGG	241 CTTCCGCCGGGTGTCATGGAGAAACTCCAGCTGGGCCCAGAGATTCTGCAGCGGGAAAA 300 [301 TCCAAGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCCGGTT 360 361 AGCTGGCCACGATATCAACTATTTGGCTTTGTCAGGTGTTCTCTCAAAAATTGGCAGAAG 420 361 AGCTGGCCACGATATCAACTATTTGGCTTTGTCAGGTGTTCTCTCAAAAATTGGCAGAAG 420	421 TGGTGAGAATCCGTATGCCCCGCTGAATCTCCTGGCTGACTTTGCTGGTGGTGGTGGCCTTAT 480	481 GTGTGCACTGGGCATTATAATGGCTCTTTTTGACCGCACACGCACTGACAAGGGTCAGGT 540 	541 CATTGATGCAAATATGGTGGAAGGAACAGCATATTTAAGTTCTTTTCTGTGGAAAACTCA 600 	601 GAAATGGAGTGTGTGGGAAGCACCTCGAGGACAACATGTTGGATGGTGGAGCACCTTT 660 	661 CTATACGACTTACAGGACAGCAGATGGGGATTCATGGCTGTTGGAGCAATAGAACCCCA 720	721 GTTCTACGAGCTGCTGATCAAAGGACTTGGACTAAAGTCTGATGAACTTCCCAATCAGAT 780 	781 GAGCATGGATTGGCCAGAAATGAAGAAGAAGTTTGCAGATGTATTTGCAAAGAAGA (840 	841 GAAGGCAGAGTGTCAAATCTTTGACGCACAGATGCCTGTGTGACTCCGGTTCTGAC 900	901 TITIGAGGAGGITGTTCATCATGATCACAAGGAACGGGGCTCGTTTATCACCAGTGA 960 	961 GGAGCAGGACGTGAGCCCCGGCCCTGCACCTCTGCTTAAACACCCCCAGCCATCCCTTC 1020	1021 TTTCAAAAGGGATCCTTTCATAGGAGAACACTGAGGAGATACTTGAAGAATTTGGATT 1080

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Publication No. US20020193296A1
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Publication No. US20020183251A1
GENERAL INFORMATION:
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Bay, Craig H.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
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TITLE OF INVENTION: COMPOSITIONS AND METHODS TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CAURING THE REPERENCE: 210121.427C26
CURRENT APPLICATION NUMBER: US/09/895,814
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 990
SECTIANARE: FRAUSEQ for Windows Version 3.0
                                                                                                                                                                                                       ; Score 1621;
; Pred. No. 0;
0; Mismatches
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Best Local Similarity 100.0%;
Matches 1621; Conservative 0
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CORGANISM: Homo sapien
US-09-895-814-107
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b; Pred. No. 0;
0; Mismatches
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Hepler, William T.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hural, John
APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Raymond L.
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APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Gary R.
APPLICANT: Wantenabe, Yoshihiro
APPLICANT: Wantenabe, Yoshihiro
APPLICANT: Macaher, Madeleine Joy
APPLICANT: Macher, DIAGNOSIS OF PROSTATE CA
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CA
FILE REFERENCE: 2011.12-10
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 107
LENGTH: 1621
                                                                                                                                                                                                                                                                                                                        Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 1621; Conservative 0;
                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-012-896-107
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                     APPLICANT: Xu, Jangchun
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APPLICANT: Harlocker, Jennifer L.
APPLICANT: Harlocker, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Red, Steven G.
APPLICANT: Kalos, Michael
APPLICANT: Redes, Michael
APPLICANT: Retter, Mark
APPLICANT: Setter, Mark
APPLICANT: Solk, John
APPLICANT: Solk, John
APPLICANT: OMPOSITIONS AND METHODS FOR THER
TITLE OF INVENTION: COMPOSITIONS AND METHODS
FILE REFERENCE: 210121.42703
CURRENT APPLICATION NUMBER: US/10/010,940
CURRENT FILING DATE: 2001-12-05
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FASTERD for Windows Version 3.0
SEQ ID NO 107
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100.0%; Score 1621;
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Publication No. US20030088062A1
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APPLICANT: HIGGERM, JUBILIEE L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, Thomas S.
APPLICANT: Odvick, Thomas S.
APPLICANT: Wang, Aijun A.
APPLICANT: Wang, Aijun A.
APPLICANT: Wang, Aijun A.
APPLICANT: Wang, Ailun T.
APPLICANT: Hural, John A.
APPLICANT: Hural, John A.
APPLICANT: Hural, John A.
APPLICANT: Wang, Skeiky, Yashir A. W.
APPLICANT: Wang, Skeiky, Yashir A.
APPLICANT: Wang, Skeiky, Yashir C.
APPLICANT: Wang, Ailliam T.
APPLICANT: Wang, Skeiky, Yashir C.
APPLICANT: Wang, Skeiky, Sashir S.
APPLICANT: Wathanbe, Yoshihiro
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CURRENT APPLICATION NUMBER: US/10/144,678A

SOFTWARE: FORESQ for Windows Version 3.0

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100.0%; Pred. No. 0;
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                                    APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Micham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Ranger, Gary R.
APPLICANT: Rocter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Thomas S.
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Matches 1621; Conservative
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ORGANISM: Homo sapiens
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GTTCTACGAGCTGCTGATCAAAGGACTTGGACTAAAGTCTGATGAACTTCCCAATCAGAT
                                         GAGCATGGATGATTGCCCAGAAATGAAGAAGATTTGCAGATGTATTTGCAAAGAAGAC
                                                                                  GAAGGCAGAGTGGTGTCAAATCTTTGACGGCACAGATGCCTGTGTGACTCCGGTTCTGAC
                                                                                               Sequence 107, Application US/11234786; Publication No. US20060024301A1; GENERAL INFORMATION: APPLICANT: Xu, Jiangchun; APPLICANT: Dillon, Davin C.
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Publication No. US20040141989A1

GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PRO:
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PRO:
TITLE REFERENCE: 210121.427D4
CURRENT FILING DATE: 2003-10-17
CURRENT FILING DATE: 2003-10-17

NUMBER OF SEQ ID NOS: 228
SOFTWARE: FREE OF COMPOUNDS FOR WINDOWS VERSION 4.0
SEQ ID NO 107
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Best Local Similarity 100.
Matches 1621; Conservative
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CORGANISM: Homo sapiens
US-10-688-838-107
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APPLICANT: Skeiky, Yasir A.
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TITLE OF INVENTION: PROSTATE-SPECIFIC POLYPEPTIDES AND FUSION
TITLE OF INVENTION: PROSTATE-SPECIFIC POLYPEPTIDES AND FUSION
FILE REFERENCE: 210121.427C31
CURRENT PELLON NUMBER: US/11/234,786
CURRENT FILING DATE: 2006-09-23
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PRIOR PELLING DATE: 2000-05-09
PRIOR FILING DATE: 2000-00-0-14
PRIOR FILING DATE: 1999-07-13
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                    Harlocker, Susan L.
Jiang, Yuqiu
Reed, Steven G.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marz W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
Li, Samuel X.
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Db 1381 AGTTATTCTGCCTTCCAGTTTGCTTGATATTTGTTGATGATTTTGACTTTATA 1440 Oy	Qy 1621 A 1621 Db 1621 A 1621 RESULT 15 15. Sequence 21284, Application US/10357930 1 Publication No. US20040259086A1	APPLICANT: Schlegel. Robert APPLICANT: Schlegel, Wilson APPLICANT: Bridge, Wilson APPLICANT: Monahan, John TILLE OF INVENTION: INDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF TILLE OF INVENTION: HUMAN PROSTATE CANCER TILLE REPERENCE: MRI-ODISCN TURENT APPLICATION NUMBER: US/10/357,930 CURRENT FILING DATE: 2003-02-04	PRIOR FILING NUMBER: 09/705,276	PRIOR APPLICATION NUMBER: 60/219,007	US-10-357-930-21284 Query Match Query Match Best Local Similarity 99.9%; Pred. No. 0; Matches 1578; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Qy 1 CGCCATGGCACTGCAGGCATCTCGGTCATGAGCTGTCCGGCCTGGCCCCGGCCCGT 60	Qy 61 CTGTGCTATGGTCCTGGCTGACTTCGGGGCGCGTGTGCTACGGGCCGGCC

Search completed: December 31, 2006, 13:56:06 Job time : 2584.16 secs

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Novel human prostate specific tumour protein and fragments - useful for detecting and treating prostate cancers.
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Maximum Match 100%
Listing first 45 summaries
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         This sequence represents a human prostate tumour specific gene, and can be used in the method of the invention. The method is for detecting prostate cancer comprises contacting a biological sample with an agent able to bind an immunogenic portion of a prostate protein (such as encoded by this sequence). An antibody which binds to an immunogenic portion of the prostate protein, and the method can be used to detect, monitor progression of, or treat prostate cancers. The antibody may also be conjugated to a therapeutic agent for use in therapy of prostate cancers. (Updated on 25-MAR-2003 to correct PR field.)
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                                                                                                                                                                                                                                         Polypeptides comprising immunogenic portions of prostate in a vaccine for the treatment of prostate cancer.
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The present invention describes polynucleotide sequences (I) which encode prostate-specific proteins (II). (I) and (II) have cytostatic activity, and can be used in vaccine production and gene therapy. (I), (II), antibodies to (II), fusion proteins comprising (II), and isolated T cells prepared using (I) or (II) are used treat cancer in a patient. (I) and the antibodies are also used in the detection of cancer in a patient. (I) and (II) can be used in vaccines. The antibodies or III can be used in vaccines. The antibodies or (II) can be used for monitoring the progression of cancer in a patient. (I) and (II) can be used to improve diagnostic and therapeutic methods for prostate cancer. They can indicate the level of metastasis as well as the prostate polynucleotide and anino acid sequences used in the exemplification of the present invention
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The invention relates to isolated prostate-specific polynucleotides, polypeptides, fusion proteins of the polypeptides, antibodies raised against the polypeptides (or antigenic epitopes derived from them) and antigen-presenting cells expressing the polypeptides. The antibodies are useful for detecting the presence of cancer, especially prostate cancer. The polypeptides, polynucleotides and the antigen-presenting cells are protein, and for inhibiting the development of cancer especially prostate cancer. Compositions comprising the polynucleotide and/or polypeptide are useful for stimulating and immune response, and for treating cancer. The oligonucleotide is useful for detecting cancer. The polygoucleotide is useful for detecting cancer. The polygoucleotide is useful for detecting cancer. The polygoucleotide is useful for detecting cancer. The prostate specific polynucleotide of the invention
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Carter D;
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09-MAY-2000; 2000US-00568100.
12-MAY-2000; 2000US-00570737.
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27-JUN-2000; 2000US-00605783.
09-AUG-2000; 2000US-00636215.
29-AUG-2000; 2000US-00651236.
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02-OCT-22000; 2000US-00679426.
10-OCT-2000; 2000US-00685166.
09-NOV-2000; 2000US-00709729.
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specific proteins and oligonucleotides that hybridise to a polynucleotide that encodes a prostate specific protein are useful for detecting the presence or absence of a cancer or monitoring the progression the progression of a cancer, especially prostate cancer. AAH02422 to AAH2872, AAB74798 to AAB74821 and AAB74830 are sequences used in the exemplification of the present invention
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                                                                                                                                                                         Prostate cancer; vaccine; gene therapy; cytostatic; fusion protein; immunogen; cancer; prostate specific antigen; PSA; prostatic acid phosphatase; PAP; prostate specific membrane antigen; PSMA; gene; ss.
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Carter D;
Hural J;
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                                                                                                                                                  Prostate cancer therapy associated cDNA #107
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                                                                       CDNA; 1621
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04-OCT-2000; 2000US-00679272.
28-MAR-2001; 2001US-00822827.
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CARTER D.
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prostate cancer. The proteins are useful as markers to indicate the presence or absence of cancer. This sequence represents a prostate cancer therapy associated CDNA. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the US patent office at seqdata.uspto.gov/sequence.html?DocID=US20020192763
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ment of
                                                                                                                           Novel polynucleotide encoding polypeptide comprising a portion of prostate tumor protein useful for inhibiting development of prostate cancer or for treating prostate cancer in a patient.
                                                                                                                                                                                              The sequence is a human prostate tumour cDNA which encodes a part tumour protein. The DNA is useful for inhibiting the development prostate cancer or for treating prostate cancer in a patient
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cancer; vaccine; cytostatic; immunostimulant;
                     Human F1-12 cDNA sequence SEQ ID NO 107.
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27-MAR-2000; 2000US-00536897.
29-MAY-2000; 2000US-00568100.
12-MAY-2000; 2000US-00570737.
13-JUN-2000; 2000US-00593793.
27-JUN-2000; 2000US-00605783.
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97US-00904804.
98US-00030607.
98US-00115453.
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98US-00158112.
99US-00288946.
99US-00432616.
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02-OCT-2000; 2000US-00679426
10-OCT-2000; 2000US-00685166
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  (first entry)
                                           Human; cancer; prostate
gene therapy; gene; ss.
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RETTER M W.
STOLK J. A.
DAY C H.
VEDVICK T S.
CARTER D.
LI S X.
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DILLON D C.
MITCHAM J L.
HARLOCKER S I
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KALOS M D.
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GR, Retter
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  19-JUL-2002
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                    GTTCTACGAGCTGCTGATCAAAGGACTTGGACTAAAGTCTGATGAACTTCCCAATCAGAT
                                                                         GAGCATGGATGATTGGCCAGAAATGAAGAAGTTTGCAGATGTATTTGCAAAGAAGAC
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                                GTTCTACGAGCTGCTGATCAAAGGACTTGGACTAAAGTCTGATGAACTTCCCAATCAGA
                                                              GAGCATGGATTGCCCAGAAATGAAGAAGTTTGCAGATGTATTGCAAAGAAGAA
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The present invention provides prostate-specific coding sequences and their encoded proteins. These can be used in the diagnosis and treatment of cancers, particularly prostate cancer. The present sequence is a cDNA described in the invention
        Kalos MD;
Carter D;
                                                                                                                                                                                                                                  New prostate-specific polynucleotides for diagnosing and treating diseases, in particular prostate cancer, and as markers for the progression of cancer.
Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
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ABL94927

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AGTTATICTGCCTICCAGTITGCTTGATATTIGTTGATATTAAGATICTTGACTIATA
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       TITCAAAAGGGATCCTITCATAGGAGAACACACTGAGGAGATACTTGAAGAATTTGGATT
                  TTTCAAAAAGGGATCCTTTCATAGGAGAACACACTGAGGAGATACTTGAAGAATTTGGATT
                                                                              AGCTAGTCTCTAACTTCCAGGCCCACGGCTCAAGTGAATTTGAATACTGCATTTACAGTG
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                   DB 6; Length 1621;
461 A; 330 C; 412 G; 418 T; 0 U; 0 Other;
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100.0%; Score 1621;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1621; Conservative 0; Mismatches
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 Sequence 1621
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The invention relates to a method of detecting prostate cancer by contacting a biological sample from a patient with: (a) a binding agent that binds to a polypeptide having an immunogenic portion of a prostate protein or its variant; (b) 2 oligomucleotide primers, where 1 of the oligomucleotides is specific for a DNA encoding the polypeptide of (a); or (c) an oligomucleotide probe specific for a DNA encoding the polypeptide of (a). The method and polypeptides are useful for diagnosing, treating, particularly by immunotherapy, monitoring the progression, and inhibiting the development of prostate cancer in a patient. The polypeptides may be used to generate antibodies useful for the diagnosis and monitoring of prostate cancer. ABSS8350-ABSS8746 represent human prostate tumour CDNA sequences of the invention
                                                                                               Detecting prostate cancer comprises contacting a sample with an agent capable of binding to a polypeptide with an immunogenic portion of a prostate protein, oligonucleotide primers or a probe specific for DNA encoding the polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1621 BP; 461 A; 330 C; 412 G; 418 T; 0 U; 0 Other;
                                                                                                                                                                                                                                Claim 1; Page 59-60; 111pp; English.
                                                  WPI; 2002-607662/65.
Dillon DC;
  Xu J,
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Onerv Match	40,74	100 0%: Score 162]: DR 6: Length 1621:	
Best Loc Matches	Local Si tes 1621;	milarity 100.0%; Pred. No. 0; Conservative 0; Mismatches 0; Indels 0	.0
λ̈́δ	н	CGCCATGGCACTGCAGGCATCTCGGTCATGGAGCTGTCCGGCCTGGCCCCGGGCCCGTT 6	90
qa	H	CGCCATGGCACGGCATCTCGGTCATGGAGCTGTCCGGCCTGGCCCCGGGCCCGTT 6	09
ò	61	CTGTGCTATGGTCCTGGCTGACTTCGGGGCGCGTGTGGTACGCGTGGACCGGCCCCGGCTC 1	120
Db	61	CTGTGCTATGGTCCTGGCTGACTTCGGGGCGCGTGTGGTACGCGTGGACCGGCCCGGCTC	120
ò	121	CCGCTACGACGTGAGCCGCTTGGGCCGGGGCAAGCGCTCGCT	180
qq	121	CCGCTACGACGTGAGCCGCTTGGGCCGGGGCAAGCGCTCGCT	180
ò	181	GCCGCGGGGGCCCCCGTGCTGCGCGCTTGCAAGCGGTCGGATGTGCTGCTGCTGCCCC	240
qq	181	GCCGCGGGGAGCCGCCGTGCGGCGTCTGTGCAAGCGGTCGGATGTGTGCTGCTGGAGCC	240
δλ	241	CTTCCGCCGCGGTGTCATGGAGAACTCCAGCTGGGCCCCAGAGATTCTGCAGCGGGAAAA 3	300
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ପ୍ପ	301	TCCAAGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCCGGTT 3	360
δ	361	AGCTGGCCACGATATCAACTATTTGGCTTTGTCAGGTGTTTCTCTCAAAAATTTGGCAGAAG	420
qa	361	AGCTGGCCACGATATCAACTATTTGGCTTTGTCAGGTGTTCTCTCAAAAATTGGCAGAAG	420
è	421	TGGTGAGAATCCGTATGCCCCGCTGAATCTCCTGGCTGACTTTGCTGGTGGTGGCCTTAT 4	480
qa	421	TGGTGAGAATCCGTATGCCCCGCTGAATCTCCTGGCTGACTTGCTGGTGGTGGCCTTAT 4	480
ò	481	GTGTGCACTGGGCATTATAATGGCTCTTTTTGACCGCACACGCACTGACAAGGGTCAGGT 5	540
qa	481	GIGGACTGGGCATTATAAAGGCTCTTTTTGACCGCACACGCACTGACAAGGGTCAGGT	540
ò	541	CATTGATGCAAATATGGTGGAAGGAACAGCATATTTAAGTTCTTTTCTGTGGAAAACTCA	009
qq	541	CTTTTCTGTGGAAACTCA	009
ò	601	GAAATCGAGTCTGTGGGAAGCACCTCGAGGACAGACATGTTGGATGGTGGAGCACCTTT	099
qq	601	GAAATCGAGTCTGTGGGAGCACCTCGAGGACGACATGTTGGATGGTGGAGCACCTTT 6	099

RESULT 13 ACC95091 ID ACC95091 standard; cDNA; 1621 BP.

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                         AGCTGGCCACGATATCAACTATTTGGCTTTTGTCAGGTGTTCTCTCAAAAATTGGCAGAAG
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Kalos MD, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS;
Carter D, Li SX, Wang A, Skeiky YAW, Hepler WT, Hural J;
Moneill PD, Houghton RL, Vinals Y De BassolsC, Foy TW, Watanabe Deng T;
                                                                                      human;
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                                                                               prostate-specific protein; PSP; cancer; ss.
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100.0%; Pred. No. 0;
ative 0; Mismatches
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                                                        specific cDNA
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29-JUN-2001; 2001US-00895814.
10-DEC-2001; 2001US-00012896.
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                                                                                      therapy; prostate
                             (first entry)
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Matches 1621; Conservative
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                                                                                                                                                                                                                                                                                                      (CORI-) CORIXA CORP.
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                                            1501 ATTTACACTCTTGATTCTACAATGTAGAAATGAGGAAAATGGCCACAAATTGTATGGTGAT 1560
                                                                    Human; 88; prostate specific cDNA; cytostatic; immunostimulant;
gene therapy; call therapy; vaccine; T-cell epitope;
class I major histocompatibility complex allele; MHC; prostate cancer;
tumour; antigen presenting cell.
            ATTTACACTCTTGATTCTACAATGTAGAAAATGAGGAAATGCCACAAATTGTATGGTGAT
                                                              Human prostate specific full length cDNA F1-12/P504S.
                                                                                                                                  ADB13557 standard; cDNA; 1621 BP
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980S-00020956-
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                                                                                       1621 A 1621
                                                                                                   A 1621
                                                                                                                                                                                                                                                                                                                                                        09-MAY-2000;
12-MAY-2000;
13-JUN-2000;
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10-OCT-2000;
09-NOV-2000;
                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                            18-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                           27-JUN-2000;
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The invention relates to an isolated polypeptide comprising no more than CC The invention relates to an isolated polypeptide comprising a sequence ADB14487. The peptides comprise a fragment ADB1363 of that contain naturally processed T-cell epitopes for 3 class I major histocompatibility complex (MHC) alleles. ADB1363 is a polypeptide encoded by a human prostate specific CDNA, one of 648 disclosed as new. Also included are nucleic acids encoding the proteins and peptides, expression vectors, a host cell cannot be proteined with the vector, an isolated antibody (or antigen binding fragment) that specifically binds to the protein or peptide, detecting a fragment) that specifically binds to the protein or peptide, detecting fragment) that specifically binds to the protein or peptide that binds to appearing as ADB1355, detecting the amount of polypeptide that binds to appearing as ADB1355, detecting the amount of polypeptide that binds to off value to determine the presence of cancer), a fusion protein comprising the presence of acontacting or expanding T cells with the appetides or protein comprising or expanding T cells with the peptides or protein comprising or expanding T cells with the peptides or the isolated T cell population, treating prostate cancer in a patient and treating prostate cancer in a patient and treating prostate cancer in a patient and treating prostate cancer in a patient the T cells proliferate, and administering the cancer in a patient. The peptides or antigen presente of cancer in a patient. The peptides (or an oligonuclectide that hybridiess to nucleic acid and administering che cancer in a patient. The peptides (or an oligonuclectide that hybridiess to nucleic acid are used to antigen contacting cells expressing the nucleic acid are used to cancer in a patient. The peptides, mucleic acid, are used to stimulate an immune response or treat presente of cancer in a patient. The peptides, mucleic acide, antibodies, fusion proteins, T cell populations or treat presenting cells are used to stim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 CTGTGCTATGGTCCTGGCTGACTTCGGGGCGCGTGGTACGCGTGGACCGGCCCCGGCTC 120
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                                                                                                                                                                                           polypeptide for use in a vaccine for stimulating an in for treating or diagnosis cancer, preferably prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 10; Length 1621;
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100.0%; Pred. No. 0;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                             Claim 19; Page; 101pp; English
Kalos MD;
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Matches 1621, Conservative
                                                                         2003-756193/71.
Stolk JA,
                                                                                                                 P-PSDB; ADB13558.
                                                                                                                                                                                           New isolated response, or
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Υ; Æ Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson F 4D, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS; D, Li SX, Wang A, Skeiky YAW, Hepler WT, Hural J; L PD, Houghton RL, Vinals Y De BassolsC, Foy TM, Watanabe Deng T; Kalos MD, F Carter D, L Mcneill PD, Meagher MJ

2003-777973/73.

P-PSDB; ADG25974

New polynucleotides encoding prostate specific polypeptides isolated a human prostate tumor cDNA library are useful to diagnose and treat cancer particularly prostate cancer

Example 1; SEQ ID NO 107; 99pp; English.

The invention relates to human prostate-specific polypeptides and the polynucleotides encoding them. The invention also relates to an isolated antibody or its antigen-binding fragment that specifically binds a polypeptide of the invention, a method of detecting cancer in a patient comprising contacting a biological sample of the patient with an agent that binds a prostate-specific polypeptide and comparing the amount of bound polypeptide comparated to a predetermined cut-off value and a fusion protein comprising a prostate-specific polypeptide. The sequences of the invention are used to diagnose and treat cancer, particularly prostate ancer. This sequence represents conding a human prostate-specific polypeptide of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at sequence.

Sequence 1621 BP; 461 A; 330 C; 412 G; 418 T; 0 U; 0 Other;

ö 120 120 180 180 240 240 300 300 360 360 420 420 480 480 540 9 9 CTGTGCTATGGTCCTGGCTGACTTCGGGGGCGCGTGTGGTACGCGTGGACCGGCCCGGCTC GCCGCGGGGAGCCGCCCTGCTGCGGCGTTGTGCTGCAAGCGGTCGGATGTGCTGCAAGCC CTTCCCCCGCGGGTGTCATGGAAAACTCCAGCTGGGCCCAGAGATTCTGCAGCGGGAAAA TCCAAGGCTTATTTATGCCAGGCTGAGTGGGTTTGGCCAGTCAGGAAGCTTCTGCCGGTT AGCTGGCCACGATATCAACTATTTGGCTTTGTCAGGTGTTCTCTCAAAAATTTGGCAGAAG GTGTGCACTGGGCATTATAATGGCTCTTTTTGACCGCACACGCACTGACAAGGGTCAGGT CATTGATGCAAATATGGTGGAAGGAACAGCATATTTAAGTTCTTTTCTGTGGAAAACTCA CGCCATGGCACTGCAGGGCATCTCGGTCATGGAGCTGTCCGGCCTGGCCCCGGGCCCGGTT CGCCATGGCACTGCAGGGCATCTCGGTCATGGAGCTGTCCGGCCTGGCCCCGGGCCCGGTT CTGTGCTATGGTCCTGGCTGACTTCGGGGCGCGTGTGGTACGCGTGGACCGGCCCCGGCTC GCCGCGGGGAGCCGCCGTGCGGCGTCTGTGCAAGCGGTCGGATGTGCTGCTGGAGCC CTTCCGCCGCGGTGTCATGGAGAAACTCCAGCTGGGCCCCAGAGATTCTGCAGCGGGAAAA TCCAAGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCCAGTCAGGAAGCTTCTGCCGGTT AGCTGGCCACGATATCAACTATTTGGCTTTGTCAGGTGTTCTCTCAAAAATTGGCAGAAG TGGTGAGAATCCGTATGCCCCGCTGAATCTCCTGGCTGACTTTGCTGGTGGTGGCCTTAT Gaps DB 10; Length 1621; ö Indels ; Score 1621; I Pred. No. 0; ; Mismatches ; 0 Query Match

Best Local Similarity 100.0%;

Matches 1621; Conservative 0; 241 61 61 121 121 181 181 241 301 301 361 361 421 421 481 481 541 셤 셤 ò g 8 6 8 8 8 q 8 B 8 g ૪ 셤 ઠે

1621

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1020 1140 1380 1380 720 720 780 840 840 900 960 960 CTATACGACTTACAGGACAGCAGATGGGGGAATTCATGGCTGTTGGAGCAATAGAACCCCA GTTCTACGAGCTGCTGATCAAAGGACTTGGACTAAAGTCTGATGAACTTCCCAATCAGAT GAAGGCAGAGTGTCTAAAATCTTTGACGGCACAGATGCCTGTGTGACTCCGGTTCTGAC TTTTGAGGAGGTTGTTCATCATGATCACAACAAGGAACGGGGCTCGTTTATCACCAGTGA GGAGCAGGACGTGAGCCCCCGCCCTCTGCTGTTAAACACCCCCAGCCATCCTTC GGAGCAGGACGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCCCAGCCATCCCTTC AGTTATTCTGCCTTCCAGTTTGCTTGATATTTGTTGATATTAAGATTCTTGACTTATA CATTGATGCAAATATGGTGGAAGGAACAGCATATTTAAGTTCTTTTCTGTGGAAAACTCA GAAATCGAGTCTGTGGGAAGCACCTCGAGGACAGAACATGTTGGATGGTGGAGCACCTTT GTTCTACGAGCTGCTGATCAAAGGACTTGGACTAAAGTCTGATGAACTTCCCAATCAGAT GAGCATGGATGATTGGCCAGAAATGAAGAAGAAGTTTGCAGATGTATTTGCAAAGAAGAC GAAGGCAGAGTGGTCAAATCTTTGACGCACAGATGCCTGTGTGACTCCGGTTCTGAC TITCAAAAGGGATCCTITCATAGGAGAACACACTGAGGAGATACTTGAAGAATTTGGATT AGCTAGTCTCTAACTTCCAGGCCCACGGCTCAAGTGAATTTGAATACTGCATTTACAGTG AGTIATICICCCTICCAGITIGCTIGATAITITGTIGATATIAAGAITCTIGACTIAIA TTTTGAATGGGTTCTAGTGAAAAGGAATGATATATTCTTGAAGACATCGATATACATTT **ATTTACACTCTTGATTCTACAATGTAGAAAATGAGGAAATGCCACAAATTGTATGGTGAT** CTATACGACTTACAGGACAGCAGATGGGGGAATTCATGGCTGTTGGAGCAATAGAACCCCA TAGAGTAACACATAACATTGTATGCATGGAAACATGGAGGAACAGTATTACAGTGTCCTA CCACTCTAATCAAGAAAGAATTACAGACTCTGATTCTACAGTGATGATTGAATTCTAAA **AATGGTTATCATTAGGGCTTTTTGATTTAAAACTTTGGGTACTTATACTAAATTATGGT** GAAATCGAGTCTGTGGGAAGCACCTCGAGGACAGAACATGTTGGATGGTGGAGCACCTTT A 1621 1141 1201 1261 1321 1381 1,561 781 196 1021 1021 1081 1081 1141 1321 1381 1441 1441 1501 1501 1621 541 661 721 781 841 841 901 961 1201 1261 601 601 661 721 901 ò 음 8 셤 ò g ò 셤 ò 셤 ð g ઠે g ò 셤 8 요 ò 셤 δ 셤 Š 셤 ઠે 원 ò g ò 셤 ð 셤 ò 셤 ò

Search completed: December 31, 2006, 12:54:19 Job time : 1261.98 secs

BF965166 602266459
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Database

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Infiltudes, non-

National Cancer Institute / National Institute of Dental Research,

National Cancer Institute / National Institute of Dental Research,

Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Unpublished (1997)

Contact: Robert Strauberg, Ph.D.

Email: Gapbs-r@mail.nih.gov, Ph.D.

Email: Gapbs-r@mail.nih.gov, Ph.D.

CDNA Library Preparation: David B. Krizman, Ph.D.

CDNA Library Preparation: David B. Krizman, Ph.D.

CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.

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CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.

CON Gattribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LiML at:

www-bio.llnl.gov/bbrp/image.image.html
                                                                                                                                                                                                                                                                                                                                                      478 bp mRNA linear EST 14-JUN-1999 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:1008916, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This read is a RESEQUENCE of a previously sequenced human clone Original clone citation: WashU-NCI EST Project
This read has been verified (found to hit its original self in the
                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
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Seg primer: -40TP from Gibco
High quality sequence stop: 431..
Location/Qualifiers
                                                                                                                          CE482447
CE283656
BE168137
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AQ782590
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AI732098.1 GI:5053233
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                                          Hominidae; Homo.
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                     186
177.2
168.6
112.4
101.4
                                                             VERSION
KEYWORDS
SOURCE
ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                 DEFINITION
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AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
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AI732098
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                                                                                                                                                                                         48236798 seqs, 27959665780 residues
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                                                    OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                         first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum Match 100%
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212.2
202
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST 13-DEC-1999
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D., Michael Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: David B. Krizman, Ph.D.

CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llni.gov/bbrp/image/image.html

Seq primer: -4nml3 fwd. ET from Amersham

High quality sequence stop: 367.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            300 CATATAACCATAGG---TATGGGAACAAAAAACATCAATCACTGTATCAATTGCCATG
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Pred. No. 5.3e-112;
0; Mismatches 12;
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/db_xref="taxon:9606"
/clone="IMAGE:1008916"
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ilarity 96.5%;
Conservative
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Matches 440;
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                          /lab_host="nHIQB"
/clone lib="NCI_CGAP_PrI"
/lone="Vector: pAMPI"; Site_1: Not1; Site_2: EccRI; lst
funce="Vector: pamping of the properties of the prostate epithelial cells. Double-stranded chap was
ligated to EccRI adaptors, 5 cycles of PCR applied to the
cDNA with an adaptor-specific primer, and the resulting
PCR product subcloned into pAMPI0 by the UDG-cloning
method (Life Technologies). Average insert size is 600
bp. NOTE: Not directionally cloned. This library was
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nc22g03.s1 NCI_CGAP_Pr1 Homo sapiens CDNA clone IMAGE:1008916, mRNA
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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1 (bases 1 to 461)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NAI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NAI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
Tumor Gene Index
Uppublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
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                                                                                                                                                                                                                                                                      stage="45 years old"
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AA225199.1 GI:1846507
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TITLE
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AA225199
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240 436

256

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120

316 180 299

496 356 929

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296

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/organism="Homo sapiens"
/mol_type="mRNA"
/dev_erage="Adult"
/dev_erage="Adult"
/clone_lib="FN0201"
/note="Organ: prosette normal; Vector: puc18; Site_1:
/note="Organ: prosette normal; Vector: puc18; Site_1:
Smal; Site_2: Smal; A mini-library was made by cloning
products derived from ORESTES PCR (U.S. Letters Parent
application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the pUC 18 vector: Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST 16-JAN-2001
mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome This sequence matry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC3&t2=RC3-FN0201-11100-011-FOS&t2=S000-11-11&t4=1)
Seq primer: puc 18 forward 478.
High quality sequence stop: 478.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
                                                                                                                                                                                                                          AGCAGGACCAGTTTGAGTGGCAACAATGCAGCAGCAGAATCAATGGAAACAACAGAATGA
                            TGCTCATTTTGTGTGTGGATAAAGTCAGGATGCCCAGGGGCCCAGAGCAGGGGGGCCTGCTTG
                                                                                                                              CTTTGGGAACAATGGCTGAGCATATAACCATAGGTTATGGGGAACAAAACAACATCAAAG
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RC3-FN0201-111100-011-£05 FN0201 Homo sapiens cDNA,
BF855163
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui,
Tissue Procurement: W. Marston, Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Genome Systems Inc., Gree Lennon, Ph.D.
CDNA Library Arrayed by: Mahington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
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//clone_lib="WIL CGAP Prl"
//note="Vector: pAWP10; Site_l: Not1; Site_2: EcoRI; 1st
Exrand cDNA was primed with oligo (dl)17 on 50 ng of
BNAse-treated, total cellular RNA obtained from
5,000-10,000 microdissected, histologically normal
prostate epithelial cells. Double-stranded cDNA was
ligated to EcoRI adaptors, 5 cycles of PCR applied to the
CDNA with an adaptor-specific primer, and the resulting
PCR product subcloned into pAMP10 by the UDG-cloning
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This read is a RESEQUENCE of a previously sequenced human clone original clone citation: National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index This read has been verified (found to hit its original self in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            237
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                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                               Hominidae; Homo.
1 (bases 1 to 447)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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nf31g01.x5 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:915408 similar to contains element MSR1 repetitive element ;, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            method (Life Technologies). Average bp. NOTE: Not directionally cloned. constructed by David Krizman."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="45 years old"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:915408"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        correct orientation)
Insert Length: 621 Std Error: (Seq primer: -400P from Gibco High quality sequence stop: 423.
                                                                                                    AI732238.1 GI:5053351
                                                                                                                                                   Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="Male"
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Unpublished (1997)
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                                                                            AI732238
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Matches 420;
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  DEFINITION
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TITLE
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SOURCE
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/dev stage="45 years old"
/lab_host="DH10B"
/lab_host="DH10B"
/clone lib="NCI CGAP Pr1"
/clone lib="NCI CGAP Pr1"
/not="Vector: pAMP10; Site_1: Not1; Site_2: ECORI; 1st
strand CDNA was primed with oligo(dT)17 on 50 ng of
DNAse-treated, total cellular RNA obtained from
5,000-10,000 microdissected, histologically normal
prostate epithelial cells. Double-stranded CDNA was
ligated to EcoRI adaptors, 5 cycles of PCR applied to the
CDNA with an adaptor-specific primer, and the resulting
PCR product subcloned into pAMP10 by the UGS-cloning
method (Life Technologies). Average insert size is 600
bp. NOTE: Not directionally cloned. This library was
constructed by David Krizman."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA225313 500 bp mRNA linear EST 20-AUG-1997 nc22g03.rl NCI_CGAP_Prl Homo sapiens cDNA clone IMAGE:1008916, mRNA
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTGCCATGAAGACTTGAGGGACCTGAATCTACCGATTCATCTTAAGGCAGCAGGACCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    151 ATTGCCATGAAGACNTNANGGACCTGAATCTACCGATTCATCTTAAGGCAGCAGGACCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91 TITGANIGGCAACAATGCAGCAGCAGAATCAAIGGAAACAACAACAATGATGCAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              248 AAAGACCAACAACGGCCTCAAAGGATCTCTTACCATGAAGGTCTCAGCTAATTCTTGGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                     57.8%; Score 373.6; DB 4; Length 447; 94.9%; Pred. No. 1.1e-100; tive 0; Mismatches 18; Indels 4.
                                                                        /db_xref="taxon:9606"
/clone="IMAGp998L052517 ; IMAGE:1008916"
                                    /organism="Homo sapiens"
Location/Qualifiers
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                                                                                                          /sex="Male"
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S. Bbert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M., Radelof, U., Schneider, D. and Korn, B.

Human UnigeneSet - RZPD3

L. Onpublished (2003)

Contact: Ina Rolfs

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany

RZPD; INAGP98L052517.

RZPD; INAGP98L052517.

RZPD; INAGP98L052517.

RZPD; INAGP98L052517.

RZPDILB; I.M.A.G. E. CDNA Clone Collection;

RZPD; INAGP98L052517.

RZPDILB; I.M.A.G. E. CDNA CloneCards(cgi-
htup://www.rzpd.de/CloneCards(cgi-
Heubnerveg 6, D-14059 Berlin, Germany

Tel: +49 30 32639 101

Fax: +49 30 32639 101

www.rzpd.de

This clone is available royalty-free from RZPD;

contact RZPD (clone@rzpd.de) for further information. Seg primer:

M13r, Primer sequence: TTTCACACAGGAAACAGCTATGAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     447 bp mRNA linear EST 04-FEB-2003 BX095604 NCI CGAP Pr1 Homo sapiens cDNA clone IMAGp998L052517 ; IMAGE:100891\overline{6}, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                      240
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                  TAGAGCAAAAGACCAACAACGGCCTCAAAGGATCTCTTACCATGAAGGTCTCAGTAATTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGAACCATGGCTGAGCATATAACCATAGG---TATGGGAACCAAAAACATCAAAGTCACT
                                                                                                              GNGCCTCACAGTATAGATCTGGTAGCAAAGAAGAAGAACAAAAAAACACTGATCTCTTTCTGC
                                                                                                                                                                                      TTGGCTAAGATGTGGGTTCCACATTAGGTTCTGAATATGGGGGGGAAGGGTCAATTTGCTC
                                                                                                                                                                                                                                                                                                                                                                                                          ATTITIGEGREAAAGTCAGGATGCCCAGGGGCCAGAGCAGGGGGGCTTTTG
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                                         Length 480;
                                                                           Indels
                                                                             23;
                                       Score 373.8; DB 2;
Pred. No. 9.7e-101;
0; Mismatches 23;
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                                       57.9%;
93.7%;
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                                                                             444; Conservative
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                                                          Similarity
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Best Local S
Matches 444
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COMMENT
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     ORIGIN
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Hominidae; Homo.

15. 1 (bases 1 to 541)

16. 2 Adams, M.D., Nierman, W., Malek, J., Shizuya, H., Simon, M. and Venter, J.C.

17. Venter, J.C.

18. Use of BAC End Sequences from CalTech Libraries for Sequence-Ready Map Building

18. Unpublished (1997)

19. Cher GSSs: CITBI-E1-2613A22.TR

19. Contact: Shaying Zhao, William Nierman, Mark Adams

19. Department of Eukaryotic Genomics

19. The Institute for Genomic Research

19. The Institute for Genomic Research

19. State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State 
                                                                                                                                                                                                                                                                                               AQS45351 541 bp DNA linear GSS 28-MAY-1999 CITBI-E1-2613A22.TF CITBI-E1 Homo sapiens genomic clone 2613A22, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: hbe@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13-21
Class: BAC ends.
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70 GTGGCAACAATGCAGCAGCAGAATCAAT-GAAACAACAGAATGATTGCAATCATTCTGTT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cell_type="sperm"
/clone_lib="Ciral-18"
/clone_lib="Ciral-18"
/note="Vector: pBeloBAC11; Site_1: EcoR1; Site_2: EcoR1;
CalTech Human BAC Library D"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81 ATGATTTTCATTATCATGTAAATCAGATCACTCAAGGGGCCAACCACCACGGGGGGCCCC
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (human)
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Best Local Similarity
Matches 418; Conserv
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VERSION
KEYWORDS
SOURCE
ORGANISM
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                                                                                                                                          Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui,
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui,
M.D., Michael Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGPP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bo.llnl.gov/bbpg/image/image.html
Seq primer: -28ml3 rev1 ET from Amersham
High quality sequence stop; 367.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone libe "NOT CGAP Prl"
/note="Vector: pAMP10; Site 1: Not1; Site 2: EcoRI; 1st
strand cDNA was primed with Oligo(dr)17 on 50 ng of
bNAse-treated, rotal cellular RNA obtained from
5,000-10,000 microdissected, histologically normal
prostate epithelial cells. Double-stranded cDNA was
ligated to EcoRI adaptors, 5 cycles of PCR applied to the
CDNA with an adaptor-specific primer, and the resulting
PCR product subcloned into pAMP10 by the UDG-cloning
method [Life Technologies). Average insert size is 600
bp. NOTE: Not directionally cloned. This library was
constructed by David Krizman."
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                              NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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94.8%; Pred. No. 1.8e-96;
live 0; Mismatches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="45 years old"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="IMAGE:1008916"
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                                                                                            Tumor Gene Index
Unpublished (1997)
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Best Local Similarity
Matches 458; Conserv
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                                 AUTHORS
TITLE
      REFERENCE
                                                                                                                     JOURNAL
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240 259

140 120

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Gaps

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AQ469231 546 bp DNA linear GSS 23-APR-1999 CITBI-E1-2601M18.TF CITBI-E1 Homo sapiens genomic clone 2601M18, genomic survey sequence.
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Map Building

Unpublished (1997)

Other GSSS: CITEL-E1-2601M18.TR

Contact: Shaying Zhao, William Nierman, Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

7712 Medical Center Dr., Rockville, MD 20850

Tel: 301 838 0208

East: 301 838 0208

Email: hbe@tigr.org

Clones are available from Research Genetics (info@resgen.com). BAC
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http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13-21
Class: BAC ends.
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                                                                                                                                                                                                                                                                                               399 AAGCCTACCTAATATCTGCTAGAGAAAAGACCAACAAC-GCCTCAAAGGATCTCTTACCA 341
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                                                                                                                                                                                                                                                                                                                                                                    340 IGAAGGTCTCAGCTAATTCTTGGCTAAGATGTGGGTTCCACATTAGGTTCTGAATATGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     463 AAACAACATCAAAGTCACTGTATCAATTGCCATGAAGACTTGAGGGACCTGAATCTACCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          523 ATTCATCTTAAGGCAGCAGGACCAGTTTGAGTGGCAACAATGCAGCAGCAGAATCAATGG
                                                                                                                                                                                                                                                                                                                                               TGAAGGTCTCAGCTAATTCTTGGCTAAGATGTGGGTTCCACATTAGGTTCTGAATATGGG
                                                                                                                                                           163 AACACTGATCTCTTTCTGCCACCCTCTGACCCTTTGGAACTCCTCTGACCTTTAGAAC
                                                                                                                                                                                                                                                     223 AAGCCTACCTAATATCTGCTAGAGAAAAGACCAACAACGGCCTCAAAGGATCTTACCA
                                                                                                                 Gaps
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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1 (bases 1 to 546)
Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H.,
Venter,J.C.
                                                               Length 456;
                                                                                                              20; Indels
                                                               Score 355; DB 1;
Pred. No. 4.3e-95;
0; Mismatches 20;
constructed by David Krizman."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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A0469231.1 GI:4653121
                                                               55.0%;
ilarity 93.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (human)
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                                                                                         Local Similarity
nes 425; Conserv
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                                                                         Query Match
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KEYWORDS
SOURCE
ORGANISM
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Is I bases 1 to 456)

Is Calcar Homo.

Is I bases 1 to 456)

Is NCI/NIDR-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Dental Research,
Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Concer Genome Anatomy Project (CGAP), Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui,
M.D., Michael Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: David B. Krizman, Ph.D.

CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.

CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.

CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.

CDNA Guencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at:

www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                        A1734072 456 bp mRNA linear EST 14-JUN-1999
nC22g03.y5 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:1008916, mRNA
sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /done lib="NCI_CGAP_Prl"
/folde="Vector: pAMP10; Site 1: Not1; Site 2: EcoRI; Ist strand cDNA was primed with oligo(dT)17 on 50 ng of bNAse-treated, total cellular RNA obtained from 5,000-10,000 microdissected, histologically normal prostate epithelial cells. Double-stranded cDNA was prigated to EcoRI adaptors, 5 cycles of PCR applied to the CDNA with an adaptor-specific primer, and the resulting method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This read is a RESEQUENCE of a previously sequenced human clone Original clone citation: WashU-NCI EST Project
This read has been verified (found to hit its original self in the
                                                                                            CTTGGCTAAGATGTGGGTTCCACATTAGGTTCTGAATATGGGGGGAAGGGTCAATTTGCT 360
                                                                                                                                                                                        CATITITGIGIGGATAAAGICAGGAIGCCCAGGGGCCAGAGCAGGGGCTGCTIGCITT 420
    CTAGAGAAAAGACCAAACAACGGCCTCAAAGGATCTCTTACCATGAAGGTCTCAGCTAATT 300
                            CTTGGCTAAGATGTGGGTTCCACATTATGTTCTGAATACAGGAGGAAGGGTCAATTTGCT 431
                                                                                                                                                                                                                                432 CACTITIGIGIGGGATAAAGACAGGATGCCCAGCGGCCAGAGCAGGGTGCTG-GTGCTTT 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                 465
                                                                                                                                                                                                                                                                                                       GGGAACAATGGCTGAGCATATAACCATAGGTTATGGGGAACAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /dev_stage="45 years old"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1008916"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  correct orientation)
Seg primer: -40RP from Gibco
High quality sequence stop: 422.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AI734072.1 GI:5055185
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AI734072
                                                 312
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ORGANISM
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AI734072/c
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VERSION
KEYWORDS
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AUTHORS
TITLE
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COMMENT
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us-09-232-880-308.rst

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(E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-911, Fax:81-45-503-910)
Clones are derived from the chimpanzee BAC library RPCI-43 This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CG891636 1inear GSS 01-SEP-2004 Ygmt24306 Yunnan snub-nosed monkey genomic BAC library Pygathrix bieti genomic clone 24306, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    366 CCAGCGAAAAAGACCAACA---GTTTCAAAGGATCTCTTACCATGAAGGCCTCAGTTAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        314 CCAC-----ATTATTCGAACCCCTCTCACCCTTTAGAACAAGCCCCACCTAACATCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               423 ACTTGCTAAGATGCGGGTTCCACATTACGTTCCTGAATATGTGGGGAAGGGTCAATTCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                /cell_type="lymphocytes"
/clone_lib="RPCI-43 Chimpanzee Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                    18;
                                                                                                                                                                                                                                                                                                                                                                                                 Length 713;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                 52.0%; Score 335.8; DB 14;
larity 82.1%; Pred. No. 3e-89;
Conservative 0; Mismatches 83; 1
                                                                                                                                                                                                                            1. .713
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="RP43-057E05.TJ"
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                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                             : pBACe3.6
: EcoRI
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                                                                                                                                                                                                                                                                                                                    /sex="male"
                                                                                                                              Sequencing: IJ
                                                                                                                                                                             R.Site 1
R.Site 2
                                                                                                                                                               Vector
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Matches 463; Conserv
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Pan troglodytes DNA, clone: RP43-057E05.TJ, genomic survey
sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          487
                     /organism="Homo sapiens"
/mol type="genomic DNA"
/db_xere="acen:9606"
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/coll.type="genomic
/coll.type="genomic
/clone lib="CTTBLE1"
/note="Vector: pBeloBAC11; Site_1: EcoRI; Site_2: EcoRI;
CalTech Human BAC Library D"
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (02-MG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
                                                                                                                                                                                                                                                                                                                                                               1 ACGATTTTCATTATCATGTAAATCGGGTCACTCAAGGGGCCCAACCACGAGCTGGGAGCCAC
                                                                                                                                                                                                                                                                                                      GGTGCCTCACTGTAGATCTGGTAGCAAGAAGAAGAACAACAACACTGATCTTTCTG
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TotoKi,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library RPCI-43
Unpublished
                                                                                                                                                                                                                                               10;
                                                                                                                                                                                                            Score 353.8; DB 11; Length 546;
Pred. No. 1.1e-94;
0; Mismatches 33; Indels 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGGAACAATGGCTGAGCGTATAAGCATAGGTAAGG 523
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GSS.
                                                                                                                                                                                                           Query Match
Best Local Similarity 90.6%;
Matches 413; Conservative (
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DEFINITION
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Matches
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AG183700
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9

196

256 180 313 240 365 300 422 482 419 542 479

538 600

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AQ199998
RPCI11-61C21.TK RPCI-11 Homo sapiens genomic clone RPCI-11-61C21,
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                                                                                                                                                                                                                                                                                     Hominidae, Homo.

I (bases 1 to 481)

Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K.,

Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C.

Unpublished (1998)

Contact: Mark Adams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: mdadams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library availability, please contact Pieter de Jong
(pieter@dejong.med.bufealo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
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                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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RPCII1 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11;
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GTATGACTTGCCATGAAGACTTGAGGACTCTGAATCAGTAAGGGCATCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 298.8; DB 11;
Pred. No. 3.6e-78;
0; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic_DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                      genomic survey sequence
                                                                                                                                                                        AQ199998.1 GI:3612197
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Best Local Similarity 89.6%;
Matches 346; Conservative C
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/cell type=
                                                                                                                                                                                                                Homo sapiens (human)
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   용
                                                                                                                                                                      L., H.L., Qian, Y.P., Yang, F.T., Nie, W.H., Chi, J.X. and Su, B. Construction and characterization of bacterial artificial chromosome (BAC) library of Yunnan snub-nosed monkey (Rhinopithecus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="Skin"
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Recombinants were transformed into DH108."
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                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Cercopithecidae; Colobinae; Pygathrix.
                                                                                                                                                                                                                                                                                                                               of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2003)
Unpublished (2003)
Contact: Xu, H.L. ; Su, B.
Key Laboratory of Cellular and Molecular Evolution
Kunming Institute of Zoology, the Chinese Academy of Sciences
32 Jiaochangdonglu, Kunming, Yunnan 650223, People's Republic
China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
fetrain="Yunnan snub-nosed monkey"
db_raxe="taxon:61621"
/clone="24306"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48.5%; Score 313.6; DB 12;
83.8%; Pred. No. 1.3e-82;
iive 0; Mismatches 61;
                                                               Pygathrix bieti (black snub-nosed monkey)
                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .533
'organism="Pygathrix bieti"
                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                    Email: xuhl@mail.kiz.ac.cn
                         GI:51792549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sex="male"
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Class: BAC ends.
                                                                               Pygathrix bieti
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394; Conserv
                           CG891636.1
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                       VERSION
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AQ726978 578 bp DNA linear GSS 14-JUL-1999
HS_5416_B2_F06_T7A RPCI-11 Human Male BAC Library Homo sapiens
genomic_clone Plate=992 Col=12 Row=L, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone lib="RPCI-11 Human Male BAC Library"
//note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
//note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
male blood DNA was isolated from one randomly chosen donor
and partially digested with a combination of EcoRI and
EcoRI Methylase. Size selected DNA was cloned into the
pBACe3.6 vector at EcoRI sites"
                                                                                                                                                457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
High Throughput Sequencing Center
High Throughput Sequencing Center
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D.
                                         Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
10449764
                    CTAGAGAAAAGACCAACAACGGCCTCAAAGGATCTCTTACCATGAAGGTCTCAGCTAATT
                                                                                                     CTTGGCTAAGATGTGGGTTCCACATTAGGTTCTGAATATGGGGGGAAGGGTCAATTTGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57; Indels
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/db_xref="taxon:9606"
/clone="Plate=992 Col=12 Row=L"
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Class: BAC ends
High quality sequence stop: 578.
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/organism="Homo sapiens"
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Plate: 992 row: L column: 12
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                                                                                                                                                                                                                                       458 CÁCTTTGTGTGCGGAT 473
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il Similarity 82.6%;
314; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hominidae, Homo.

1 (bases 1 to 474)

Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,

Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                      GGCTAAGATGTGGGTTCCACATTAGGTTCTGAATATGCGGNGAAGGGTCAATTTGGTCAC 455
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GGCTAAGATGTGGGTTCCACATTAGGTTCTGAATATGGGGGAAGGGTCAATTTGCTCAT 363
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
10449764
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
Ninversity of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3070 row: D column: 17
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/db_xref="taxon:9606"
/clone="Plate=3070 Col=17 Row=D"
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Pred. No. 3.5e-76;
0; Mismatches 29
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                                                                                TTTGTGTGTGATAAAGTCAGGATGC 389
                                                                                                           High quality sequence stop: 474. Location/Qualifiers
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AQI71162.1 GI:3568529
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Best Local Similarity 89.9%;
Matches 338; Conservative
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1 (bases 1 to 407)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Heler, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and Hood, L.
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                                                                                                                                                                                                                                                                                                                                                                                                                             CTAGAGAAAAGACCAACAACGGCCTCAAAGGATCTCTTACCATGAAGGTCTCAGCTAATT 300
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ACGATTTTCATTATCATGTGAATCAGATCACTCAAGGGGCCAACCACACTGGGAGCCAC 225
                                                                                                                    TGAT-AGGGGAAGGCTCATATGGGACTATCTACTGCCTAAAGTTCAACACAGGAAATAAA 284
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Fax: (206) 616-3618

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Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="plate=809 Col=4 Row=N"
/sex="male"
/clone_lib="RPCI-11 Human Male BAC Library"
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High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stop: 407.
Location/Qualifiers
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GSS.
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Homo sapiens
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DEFINITION
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AQ598346
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
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/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"
                                                                                                                                                                             3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         305
                                                                                                                                                                                                                                               137 TCATGGCAAGGTTCATACGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAAAGGT 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   244 GAGAAAAGACCAACAACGGCCTCAAAGGATCTCTTACCATGAAGGTCTCAGCTAATTCTT
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                                                                                                                                                                             12;
                                                                                                                                        DB 11; Length 407;
                                                                                                                                                                             Indels
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                                                                                                                                      Score 232.2; DB 11;
Pred. No. 3.8e-58;
0; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: December 31, 2006, 19:30:44
                                                                                                                                      Query Match
Best Local Similarity 86.2%;
Matches 294; Conservative (
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Sequence 552, App Sequence 552, App Sequence 552, App Sequence 552, App

Sequence 5 Sequence 5 Sequence 5 Sequence 5

Sequence 552, Sequence 14, Sequence 14

646

Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Post-processing:

Total number of

Searched:

27404, 27951,

Sequence Sequence Sequence Sequence Sequence 1161369, Sequence 587040, Sequence 1200449,

Sequence

Sequence 893115, Sequence 893115, Sequence 721218, Sequence 721218, Sequence 489987,

Sequence 241350, Sequence 241351, Sequence 241352

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APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C23
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSEQ for Windows Version 3.0
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6 US-11-230-251-14
2 US-10-301-480-547960
2 US-10-301-480-151369
2 US-10-301-480-1200449
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US-09-925-065A-489987
US-09-925-065A-489987
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US-10-301-480-241352
US-10-357-930-25779
US-10-357-930-27378
US-10-357-930-274604
US-10-357-930-27951
US-09-759-143-552
US-09-822-827-552
US-09-895-793-552
US-09-895-793-552
US-10-012-896-552
US-10-012-896-552
US-10-012-896-552
US-10-144-678A-552
US-10-294-625-552
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 1
US-09-759-143-308
; Sequence 308, Application US/09759143
; Patent No. US20020022248A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ION: (1)...(647)
INFORMATION: n = A, T, C or G
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Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
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Dillon, Davin C.
Mitcham, Jennifer L.
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Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
Li, Samuel
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LOCATION: (1)...(647)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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           December 31, 2006, 12:22:01; Search time 1030.23 Seconds (without alignments) 7716.790 Million cell updates/sec
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Sequence 21578,
Sequence 22089,
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Sequence 21476,
Sequence 21536,
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Sequence 308,
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                            GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-10-357-930-21562
US-10-357-930-21578
US-10-357-930-22089
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US-09-780-669-308
US-09-232-887-308
US-09-232-880-308
US-09-895-914-308
US-10-012-896-308
US-10-010-940-308
US-10-144-678A-308
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                 - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
                                                                                                                                                                                                                                                                                                   Length 647;
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100.0%; Pred. No. 2.7e-201;
tive 0; Mismatches 0;
       COMPOSITIONS AND METHODS FOR DIAGNOSIS OF PROSTATE CANCER
       TITLE OF INVENTION: COMPOSITIONS AND METHO
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE
FILE REFERENCE: 210121.427C24
CURRENT APPLICATION NUMBER: US/09/780,669
CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
SOFTWARE: FASELSEQ for Windows Version 3.0
SEQ ID NO 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 308, Application US/09822827
Sequence 308, Application US/09822827
SENERAL INPORMATION:
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND
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                                                                                                                                                                                                                              // LOCATION: (1)...(647)
// OTHER INFORMATION: n = A,T,C or
US-09-780-669-308
                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 647; Conservative
                                                                                                                                                                                               FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapien
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              Pred. No. 2.7e-201;
Mismatches 0;
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Patent No. US20020051977A1
GENERAL INFORMATION:
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Hepler, William
Hural, John
McNeill, Patricia D.
Houghton, Raymond L.
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Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
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Vedvick, Thomas S
Carter, Darrick
Li, Samuel
                               647; Conservative
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               Similarity
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US-09-780-669-308
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NAME/KEY: misc feature
                                                                                                            TYPE: DNA
ORGANISM: Homo sapien
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100.0%; Score 646; DB 3; L
Best Local Similarity 100.0%; Pred. No. 2.7e-201;
Matches 647; Conservative 0; Mismatches 0;
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER FILE REFREENCE: 210121.53401
CURRENT APPLICATION NUMBER: US/09/822,827
CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 982
SEQ ID NO 308
LENGTH: 647
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer Lynn
                                                                                                                                     NAME/KEY: misc_feature; LOCATION: (1)...(647); CTHER INFORMATION: n = A,T,C or usc.05-822-877-308
                                                                                                              ORGANISM: Homo sapien
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TITLE OF INVENTION: COMPOUNDS FOR IMMUNDIAGNOSIS OF
TITLE OF INVENTION: PROSTATE CANCER AND METHODS FOR THEIR
FILE REFERENCE: 210121.42932,880
CURRENT APPLICATION NUMBER: US/09/232,880
CURRENT FILING DATE: 1999-01-15
SOFTWARRE: FastSEQ for Windows Version 3.0
SEQ ID NO 3.08
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Pred. No. 2.7e-201;
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100.0%; Score 646; D
Best Local Similarity 100.0%; Pred. No. 2.7
Matches 647; Conservative 0; Mismatches
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; OTHER INFORMATION: n = A,T,C or US-09-232-880-308
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541 GGACCAGTTTGAGTGGCAACAATGCAGCAGAGAATCAATGGAAACAACAACAATGATTGC 600
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Hural, John
APPLICANT: Houghton, Raymond L.
APPLICANT: Vanelil, Parricia D.
APPLICANT: Vanels de Bassols, Carlota
APPLICANT: Vanels de Bassols, Carlota
APPLICANT: Panger, Gary R.
APPLICANT: Panger, Gary R.
APPLICANT: Panger, Gary R.
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100.0%; Score 646; DB 3; L
Best Local Similarity 100.0%; Pred. No. 2.7e-201;
Matches 647; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 308, Application US/09895814, Publication No. US20020193296A1, GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LOCATION: (1)...(647)
; OTHER INFORMATION: n = A,T,C or G
US-09-895-814-308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Xu, Jiangchun APPLICANT: Dillon, Davin C. APPLICANT: Mitcham, Jennifer L. APPLICANT: Harlocker, Susan L. APPLICANT: Jiang, Yuqiu APPLICANT: Ralos, Michael D. APPLICANT: Ralos, Michael D. APPLICANT: Stolk, John A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
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                                                                                                    APPLICANT: Retter, Marca W.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Houghton, Raymond L.
APPLICANT: Winals de Bassols, Carlota
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Panger, Gary R.
APPLICANT: Panger, Gary C.
APPLICANT: Ponger, Gary
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.5342
CURRENT APPLICATION NUMBER: US/09/895,793
CURRENT APPLICATION NUMBER: US/09/895,793
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSEQ for Windows Version 3.0
EENGTH: 647
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100.0%; Score 646; DB 3; Length 647;
Best Local Similarity 100.0%; Pred. No. 2.7e-201;
Matches 647; Conservative 0; Mismatches 0; Indels
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; OTHER INFORMATION: n = A,T,C or G
US-09-895-793-308
        Mitcham, Jennifer L.
                                Harlocker, Susan L.
Jiang, Yuqiu
Kalos, Michael D.
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NAME/KEY: misc feature
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APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Harlocker, Susan Louise
APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Reeter, Michael
APPLICANT: Retter, Mark
APPLICANT: Retter, Mark
APPLICANT: ROLE, John
APPLICANT: OCHOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
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                                                                                                                 100.0%; Score 646; DB 6; I
100.0%; Pred. No. 2.7e-201;
ive 0; Mismatches 0;
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US-10-010-940-308
Sequence 308, Application US/10010940
Publication No. US20030088062A1
GENERAL INFORMATION:
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 123
; OTHER INFORMATION: n = A,T,C or
US-10-012-896-308
                                                                                                             Query Match
Best Local Similarity 100.
Matches 647; Conservative
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   CCACCCCTCTGACCCTTTGGAACTCCTCTGACCCCTTTAGAACAAGCCTAATATCTG
                                                                             CTAGAGAAAAGACCAAACGGCCTCAAAGGATCTCTTACCATGAAGGTCTCAGCTAATT
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APPLICANT: Wantanabe, Yoshihiro
APPLICANT: Wantanabe, Yoshihiro
APPLICANT: Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C27
CURRENT APPLICATION NUMBER: US/10/012,896
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: FastSEQ for Windows Version 3.0
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Houghton, Raymond L.
Vinals de Bassols, Carlota
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Glang, Michael D.
APPLICANT: Stolk, Michael D.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Carter, Marc W.
APPLICANT: Carter, Thomas S.
APPLICANT: Carter, Thomas S.
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Skeiky, Yasir A.W.
Hepler, William T.
Henderson, Robert A.
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ORGANISM: Homo sapiens
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LENGTH: 647
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100.0%; Score 646; DB 6; Length 6
Best Local Similarity 100.0%; Pred. No. 2.7e-201;
Matches 647; Conservative 0; Mismatches 0; Indels
FILE REFERENCE: 210121,427D3
CURRENT APPLICATION NUMBER: US/10/010,940
CURRENT FILING DATE: 2001-12-05
NUMBER OF SEQ ID NOS: 575
SOFTWARE: PASISEQ for Windows Version 3.0
SEQ ID NO 308
LENGTH: 647
                                                                                                                        NAME/KEY: misc_feature

| LOCATION: (1)...(647)

| OTHER INFORMATION: n = A,T,C or G

US-10-010-940-308
                                                                                     TYPE: DNA
ORGANISM: Homo sapien
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US-10-144-678A-308

Sequence 308, Application US/10144678A

POLICATION No. US20030157089A1

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

APPLICANT: Dillon, Davin C.

APPLICANT: Mitcham, Jennifer L.

APPLICANT: Harlocker, Susan L.

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APPLICANT: Hural, John
APPLICANT: Hural, John
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals y de Bassols, Carlota
APPLICANT: Vinals y de Bassols, Carlota
APPLICANT: Poy, Teresa M.
APPLICANT: Poy, Teresa M.
APPLICANT: Deng, TB.
APPLICANT: Deng, TB.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
TITLE OF INVENTION: UNDARRE: US/10/144,678A
CURRENT APPLICANT: 2002-08-12
NUMBER OF SEQ ID NOS: 1033
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 308
LENGTH: 647
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100.0%; Score 646; DB 7; Length 647;
Best Local Similarity 100.0%; Pred. No. 2.7e-201;
Matches 647; Conservative 0; Mismatches 0; Indels 0
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                                                   Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
Li, Samuel X.
                                                                                                                                                                                               Skeiky, Yasir A. W
Hepler, William T.
Jiang, Yuqiu
Henderson, Robert
Kalos, Michael D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: 123
                                                                                                                                                                                Wang, Aijun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMAT.
US-10-144-678A-308
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CURRENT APPLICATION NUMBER: US 09/568,857
FILE REPLICATION NUMBER: US 09/568,857
FRIOR APPLICATION NUMBER: US 09/586,857
FRIOR FILING DATE: 2000-05-09
FRIOR FILING DATE: 1999-11-12
FRIOR APPLICATION NUMBER: US 09/439,313
FRIOR FILING DATE: 1999-11-12
FRIOR APPLICATION NUMBER: US 09/352,616
FRIOR PILING DATE: 1999-07-13
FRIOR PILING DATE: 1999-07-13
FRIOR PILING DATE: 1999-07-13
FRIOR PILING DATE: 1999-07-13
FRIOR PILING DATE: 1999-07-14
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FRIOR FILING DATE: 1999-07-14
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FRIOR FILING DATE: 1999-02-25
FRIOR FILING DATE: 1999-02-25
FRIOR FILING DATE: 1999-02-25
FRIOR FILING DATE: 1999-02-25
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                                                        TGTATCAATTGCCATGAAGACTTGAGGGACCTGAATCTACCGATTCATCTTAAGGCAGCA
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; OTHER INFORMATION: n = A,T,C or G
US-11-234-786-308
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Jiang, Yuqiu
Reed, Steven G.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
Li, Samuel X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
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ORGANISM: Homo sapien
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LENGTH: 647
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TGTATCAATTGCCATGAAGACTTGAGGGACCTGAATCTACCGATTCATCTTAAGGCAGCA
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Publication No. US20030185830A1

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun A.

APPLICANT: Xu, Jiangchun A.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

FILE REFERENCE: 210121.427C29

CURRENT APPLICATION NUMBER: US/10/294,025

CURRENT FILING DATE: 2002-11-12

NUMBER OF SEQ ID NOS: 1038

SOCTUMARE: PRESENCE FOR Windows Version 3.0

SEQ ID NO 308

LENGTH: 647
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Best Local Similarity 100.0%; Pred. No. 2.7e-201;
Matches 647; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; LOCATION: 123 -
; OTHER INFORMATION: n = A,T,C or
US-10-294-025-308
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                 RESULT 10
US-10-294-025-308
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                                                                        ACGATTTTCATTATCATGTAAAATCGGGTCACTCAAGGGGCCAACCACCAGGTGGAGCCAC
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                             Gaps
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; Publication No. US2030185830A1
; GENERAL INFORMATION:
   APPLICANT: Ku, Jiangchun A.
   APPLICANT: Stolk, John A.
   APPLICANT: Kalos, Michael D.
   TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
   TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
   FILE REFERENCE: 210121.42729
   CURRENT APPLICATION NUMBER: US/10/294,025
   CURRENT FILING DATE: 20022-11-12
   NUMBER OF SEQ ID NOS: 1038
   SOFTHARE: PESECRE FOR Windows Version 3.0
   SSEC ID NO 1034
   LENGTH: 2577
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  Length 647;
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100.0%; Score 646; DB 16;
100.0%; Pred. No. 2.7e-201;
ive 0; Mismatches 0;
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Pred. No. 4.5e-186;
0; Mismatches 8;
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Best Local Similarity 98.1%;
Matches 629; Conservative
              Best Local Similarity 100.
Matches 647; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Homo sapiens
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US-10-294-025-1034
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  Query Match
Best Local 8
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GURLEALL INFORMATION:

APPLICANT: Schlegel. Robert

APPLICANT: Schlegel. Robert

APPLICANT: Schlegel. Robert

APPLICANT: Endege, Wilson

TITLE OF INVENTION: HOWEL GENES, COMPOSITIONS, KITS, AND METHODS FOR

TITLE OF INVENTION: HUMAN PROSTATE CANCER

TITLE OF INVENTION: HUMAN PROSTATE CANCER

TITLE OF INVENTION: UNBER: US/10/357,930

CURRENT APPLICATION NUMBER: US/10/357,930

CURRENT APPLICATION NUMBER: 00/785,276

PRIOR PELING DATE: 2003-02-16

PRIOR PELING DATE: 2000-02-16

PRIOR APPLICATION NUMBER: 60/183,319

PRIOR PILING DATE: 2000-03-16

PRIOR FILING DATE: 2000-03-16

PRIOR FILING DATE: 2000-05-25

PRIOR FILING DATE: 2000-05-25

PRIOR PILING DATE: 2000-06-09

PRIOR APPLICATION NUMBER: 60/219,007

PRIOR PILING DATE: 2000-07-18

PRIOR PILING DATE: 2000-07-18

PRIOR PILING DATE: 2000-07-18

PRIOR FILING DATE: 2000-07-18

PRIOR PILING DATE: 2000-07-18

PRIOR FILING DATE: 2000-07-18
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  TGCTCAGGGGAAGGTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAAA
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1.1e-185;
nes 9;
        FILE REFERENCE: MAL-UOUNCN,
CURRENT APPLICATION NUMBER: US/10/357,930
CURRENT FILING DATE: 2003-02-04
PRIOR PLING DATE: 2003-02-16
PRIOR PLING DATE: 2003-02-16
PRIOR PLING DATE: 2000-02-16
PRIOR PLING DATE: 2000-02-17
PRIOR PLING DATE: 2000-03-16
PRIOR PLING DATE: 2000-03-16
PRIOR FILING DATE: 2000-03-16
PRIOR FILING DATE: 2000-03-16
PRIOR FILING DATE: 2000-05-25
PRIOR PLING DATE: 2000-06-09
PRIOR PLING DATE: 2000-06-09
PRIOR PLING DATE: 2000-07-18
PRIOR PLING DATE: 2000-07-18
PRIOR PLING DATE: 2000-07-18
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PRIOR PLING DATE: 2000-07-18
PRIOR PLING DATE: 2000-07-18
PRIOR PLING DATE: 2000-07-18
PRIOR PLING DATE: 2000-07-18
PRIOR PLING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 62232
SOFTWARE: FASTSEQ FOR WINDOWS VERSION 4.0
SERNGTH: 1481
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LOCATION: 1, 2, 3, 4

CTHER INFORMATION: n = A,T,C or

US-10-357-930-21536
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Matches 628; Conservative
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ORGANISM: Homo sapiens
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Sequence 21536, Application US/10357930

Publication No. US20040259086A1

GENERAL INFORMATION:
APPLICANT: Schlegel. Robert

APPLICANT: Endege, Wilson
APPLICANT: Monahan, John
TILLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: HUMAN PROSTATE CANCER

TITLE OF INVENTION: HUMAN PROSTATE CANCER
                                                                                                                                                                                                                                                                                                                                                                                                        61 TGCTCAGGGGAAGGTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAAA
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                NUMBER OF SEQ ID NOS: 62232
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 21476
LENGTH: 1481
                                                                                                                                                                                           Ö
                                                                                                                                                NAME/KEY: misc_feature; LOCATION: 1, 2, 3, 4; COTHER INFORMATION: n = A,T,C or US-10-357-930-21476
PRIOR FILING DATE: 2000-12-13
                                                                                                                                                                                                                                               Query Match
Best Local Similarity 98.0
Matches 628; Conservative
                                                                                                              ORGANISM: Homo sapiens
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; LOCATION: 1, 2, 3, 4
; OTHER INFORMATION: n = A,T,C or G
US-10-357-930-21562
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ORGANISM: Homo sapiens
                                                                                                                                    RESULT 15
US-10-357-930-21562/c
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Search completed: December 31, 2006, 13:56:01 Job time : 1032.23 secs

Sequence 534, App Sequence 1606, Ap Sequence 10070, A Sequence 1072, Ap Sequence 2014, A Sequence 2012, Ap Sequence 2012, Ap Sequence 2477, Ap Sequence 9, Appli Sequence 11251, Sequence 311, App Sequence 321, App Sequence 321, App Sequence 22119, A Sequence 22119, A Sequence 22119, A Sequence 22119, A Sequence 22170, A Sequence 22183, A Sequence 22183, A Sequence 22183, A Sequence 22183, A Sequence 22183, A Sequence 22183, A Sequence 22183, A Sequence 22183, A Sequence 22183, A

0 US-11-073-360-1606 US-11-371-354-10070 US-11-371-354-10070 US-10-612-783-1529 US-11-218-305-1072 US-11-266-748A-153623 US-11-266-748A-153623 US-11-266-748A-153623 US-11-266-748A-153623 US-11-174-307B-2477 US-11-1056-355B-101312 US-11-1056-355B-101312 US-11-1056-355B-17911 US-11-266-748A-19970 US-11-266-748A-237140 US-11-266-748A-237140 US-11-266-748A-237140 US-11-266-748A-237140 US-11-266-748A-237140

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Sequence 128, App

ALIGNMENTS

us-09-232-880-308.rnpbn

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Sequence 552, App
Sequence 1570, Ap
Sequence 221, App
Sequence 75529, A
Sequence 407591,
Sequence 478637,
Sequence 1, Appli
Sequence 214211,
Sequence 7676, A
                                                                                                                                       December 31, 2006, 12:26:03; Search time 222.451 Seconds (without alignments) 6266.684 Million cell updates/sec
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-11-056-358-75529
US-11-266-748A-407591
US-11-266-748A-478637
US-11-266-748A-14211
US-11-266-748A-6796
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AND

Sequence 145, App Sequence 155, App Sequence 23957, A Sequence 23957, A Sequence 19300, A Sequence 19377, A Sequence 19377, A Sequence 25041, A

US-11-266-748A-215548 US-10-449-902-19300

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US-11-056-355B-46304 US-11-454-296-35 US-11-266-748A-23957

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          PRIOR FILING DATE: 2001-01-12
PRIOR FILING DATE: 2000-11-09
PRIOR FILING DATE: 2000-11-09
PRIOR PILING DATE: 2000-11-09
PRIOR PLING DATE: 2000-11-09
PRIOR PLING DATE: 2000-10-00
PRIOR APPLICATION NUMBER: 09/679,426
PRIOR APPLICATION NUMBER: 09/679,279
PRIOR APPLICATION NUMBER: 09/657,279
PRIOR APPLICATION NUMBER: 09/657,279
PRIOR PILING DATE: 2000-09-06
NUMBER OF SEQ ID NOS: 1033
SOFTWARE: PARISE (FOR Windows Version 3.0)
SEQ ID NO 308
LENGTH: 647
APPLICATION NUMBER: 09/759,143
                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY: misc_feature
; LOCATION: 123
; OTHER INFORMATION: n = A,T,C or G
US-11-344-932-308
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Best Local Similarity 100.0
Matches 647; Conservative
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ORGANISM: Homo sapiens
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636 ACGATTTTCATTATCATGTAAATCGGGTCACTCAAGGGGCCAACCACACGTGGGAGCCAC 695
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APPLICANT: Watanabe, Yoshihiro
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Meagner, Madeleine Joy
APPLICANT: Meagner, Madeleine Joy
APPLICANT: Deng, Ta
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427732
CURRENT APPLICATION NUMBER: 10/144,932
CURRENT FILING DATE: 2006-02-01
PRIOR FILING DATE: 2002-05-09
PRIOR FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: 09/855,911
PRIOR PLILNG DATE: 2001-06-29
PRIOR PRILNG DATE: 2001-06-29
PRIOR PLILNG DATE: 2001-06-29
PRIOR PLILNG DATE: 2001-05-09
PRIOR PLILNG DATE: 2001-01-05
PRIOR PLILNG DATE: 2001-01-05
PRIOR PLILNG DATE: 2001-01-05
PRIOR PLILNG DATE: 2001-01-02
PRIOR PLILNG DATE: 2001-01-02
PRIOR PLILNG DATE: 2001-01-02
PRIOR PLILNG DATE: 2000-01-09
PRIOR PLILNG DATE: 2000-01-09
PRIOR PLILNG DATE: 2000-01-06
PRIOR PLILNG DATE: 2000-01-06
PRIOR PLILNG DATE: 2000-01-06
PRIOR PLILNG DATE: 2000-01-06
PRIOR APPLICATION NUMBER: 09/651,279
PRIOR PLILNG DATE: 2000-01-06
PRIOR APPLICATION NUMBER: 09/657,279
PRIOR APPLICATION NUMBER: 09/657,279
PRIOR APPLICATION NUMBER: 09/657,279
PRIOR PLILNG DATE: 2000-01-06
PRIOR APPLICATION NUMBER: 09/657,279
PRIOR APPLICATION NUMBER: 09/657,279
PRIOR PLILNG DATE: 2000-01-06
PRIOR APPLICATION NUMBER: 09/657,279
PRIOR APPLICATION NUMBER: 09/657,279
PRIOR PLING DATE: 2000-00-06
PRIOR APPLICATION NUMBER: 09/657,279
PRIOR APPLICATION NUMBER: 09/657,279
PRIOR PLING DATE: 2000-00-06
PRIOR APPLICATION NUMBER: 09/657,279
PRIOR PLING DATE: 2000-00-06
PRIOR APPLICATION NUMBER: 09/657,279
PRIOR PRINGRE PRESED FOR WINDOW VERSION 3.0
SOFTWARE: PRESED FOR WINDOW VERSION 3.0
SOFTWARE: PRESED FOR WINDOW VERSION 3.0
SOFTWARE: PRESED FOR WINDOW VERSION 3.0
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98.0%; Pred. No. 8.8e-189;
tive 0; Mismatches 9;
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McNeill, Patricia D.
Houghton, Raymond L.
Vinals y de Bassols, Carlota
Application US/11344932
5. US20060269532A1
                                                                                               APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Fanger, Gary R.
APPLICANT: Forger, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Skeiky, Yasir A. W.
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Best Local Similarity 98.0
Matches 628; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Li, Samuel X.
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; ORGANISM: Homo sapiens
US-11-344-932-552
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Sequence 552, Applic
Publication No. US2
GENERAL INFORMATION
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1372 GAGGCTAAAGGTAGGATGAAGGAAAGGAAACCGGGTTTGGCAGATTGCTTTTGGAAGTGGG 1431
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                                            TTGGGAACAATG
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                                                                                                                                                                                                                                                                                                          APPLICANT: BROVER, Vyacheslav
TITLE OF INVENTION: UNCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THER
TITLE OF INVENTION: USEFUL FOR MODIFYING PLANT CHARACTERISTICS
FILE REFERENCE: 2750-16019022
CURRENT APPLICATION NUMBER: US/11/174,307B
CURRENT FILING DATE: 2005-06-30
PRIOR APPLICATION NUMBER: 60/583,671
PRIOR FILING DATE: 2004-06-30
PRIOR APPLICATION NUMBER: 60/583,651
PRIOR FILING DATE: 2004-06-30
PRIOR PILING DATE: 2004-06-30
PRIOR PILING DATE: 2004-06-30
PRIOR PILING DATE: 2004-06-30
PRIOR PILING DATE: 2004-06-30
PRIOR POSS SEQ ID NOS: 5544
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Pred. No. 0.31;
0; Mismatches 69;
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i_LOCATION: (1)...(1566)
cother lineRwAtion: Also known as Ceres CDNA ID
US-11-174-307B-221
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US-11-056-355B-75529
; Sequence 75529
; Sequence 75529
; Sequence 75529
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA F);
; TITLE OF INVENTION: Polypeptides Encoded Thes;
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
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                                                                                                                                                                                                                                 Sequence 221, Application US/11174307B; Publication No. US20060143729A1; GENERAL INFORMATION: APPLICANT: ALEXANDROV, Nickolai; APPLICANT: BROVER, Vyacheslav
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Arabidopsis thaliana
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Best Local Similarity 53.1<sup>5</sup>
Matches 78, Conservative
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OTHER INFORMATION: Ceres
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US-11-174-307B-221
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                                                                CTAGAGAAAAGACCAACAACGGCCTCAAAGGATCTCTTACCATGAAGGTCTCAGCTAATT
                                                                                                                                                                                                                                                                                                  CTTGGCTAAGATGTGGGTTCCACATTAGGTTCTGAATATGGGGGGAAGGGTCAATTTGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1570, Application US/1028444
Publication No. US20060188875A1
GENERAL INFORMATION:
APPLICANT: Cox, David
APPLICANT: Patil, Nila
APPLICANT: Hinds, Anthony
APPLICANT: Hinds, David
TITLE OF INVENTION: Human Genomic Polymorphisms
FILE REFERENCE: 2001/1013-11
CURRENT APPLICATION NUMBER: US/10/284,444
CURRENT FILING DATE: 2002-10-31
PRIOR PILLING DATE: 2001-09-18
NUMBER OF SEQ ID NOS: 37858
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64.8%; Pred. No. 4.5e-09;
tive 1; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn version 3.3
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Best Local Similarity 64.8'
Matches 118; Conservative
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; ORGANISM: Homo sapiens
US-10-284-444-1570
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US-10-284-444-1570
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                                                                                                           400 GAGCAGGGGGCTGCTTGCGTAACAATGGCTGAGCATATAACCATAGGTTATGGGGA 459
                                                                                                                                                                                                                      460 ACAAAACAACATCAAAGTCACTGTATCAATTGCCATGAAGACTTGAGGGACCTGAATCTA 519
                                                                                                                                                                                                                                                                                                                                                                        900 gaccaagaggccacarargagaarcacagarraagcraaaarccaraagaagracarc 841
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                                                           Gaps
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APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
FILE REPERENCE: 55815-0102 (319189)
FILE REPERENCE: 55815-0102 (319189)
FILE REPERENCE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105492.6
PRIOR PRILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR PELLING DATE: 2004-11-03
PRIOR FILING DATE: 2005-03-14
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Score 36; DB 6; Length 1145;
Pred. No. 0.41;
0; Mismatches 105; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , Sequence 407591, Application US/11266748A ; Publication No. US20060134663A1
                                                                                                                                                                                                                                                                                                                                                                                                                                               580 IGGAAACAACAGAAIGAIIGCAAI 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               720 rccaagcacaarrgrggcarcagr 697
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    257 recererceacacacir 241
        5.6%;
  Query Match
Best Local Similarity 48.59
Matches 99; Conservative
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US-11-266-748A-407591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Harkin, Paul
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Best Local Similarity
Matches 51; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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US-11-266-748A-478637
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APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION:
SEQUENCE DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: 105/10/953,349
CURRENT PAPLICATION NUMBER: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 1766
LENGTH: 1145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1432 TTTAAGTGTAACÁGTGCAGTTTGGGTGGCTCTAAACAATGTCAAGCCTTCGGTTAGTATC 1491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   371 GTGGATAAAGTCAGGATGCCCAGGGGCCAGAGCAGGGGCTGCTTGCGTACAATG 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)._[1566]
OTHER INFORMATION: Ortholog of Ceres SEQ ID NO 13503610
OTHER INFORMATION: as cited in SEQ ID NO 62416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)._(1566)
OTHER INFORMATION: Ortholog of Ceres SEQ ID NO 13657610
OTHER INFORMATION: as cited in SEQ ID NO 66165
                                                                                                                                                                                                                                                                                                                                       LOCATION: (1). T(1566)
OTHER INFORMATION: Ortholog of Ceres SEQ ID NO 15175923
OTHER INFORMATION: as cited in SEQ ID NO 54037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (1). T(1566)
OTHER INFORMATION: Ortholog of Ceres SEQ ID NO 13598312
OTHER INFORMATION: as cited in SEQ ID NO 68448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of Ceres SEQ ID NO 13596100
in SEQ ID NO 68573
                                                                                                                                                                                                     NAME/KEY: misc feature
LOCATION: (1). (1566)
OTHER INFORMATION: Ceres Seq. ID no. 6443376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1492 CGTGGGAACACTGCATCGACCGATATC 1518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         491 GCCATGAAGACTTGAGGGACCTGAATC 517
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US-10-953-349-1766/c
; Sequence 1766, Application US/10953349
; Publication No. US20060107345A1
                                                                                                     TYPE: DNA
ORGANISM: Arabidopsis thaliana
PEATURE:
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; ORGANISM: Arabidopsis thaliana
US-10-953-349-1766
           PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 75529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (1). (1566)
OTHER INFORMATION: Ortholog
OTHER INFORMATION: as cited
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NAME/KEY: misc_feature
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LOCATION: (1)..(1566)
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50371 TAACATTAAGACAGTTTCACTCAGGAAACCAAACAGAACTTAGACAAATGCTTAGAAGC 50312
                                                                                                                                                                                                                                                     50311 ACATGGAGACGAGCCTTTATGCTTCTCAAGGCCAACTCACTAATCCATCAGTTAATGAAT 50252
                             ö
                                                                                                                                                                                                72 AGGTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAAAGGNGCCTCACA 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    407 GGGCTGCTTTGGGAACAATGGCTGAGCATATAACCATAGGTTATGGGGAACAAAAC 466
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                                                                                    12 TATCATGTAAATCGGGTCACTCAAGGGGCCCAACCACAGGTGGAGGCCACTGCTCAGGGGA
                                Gaps
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                                73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 8;
                                                                                                                                                                                                                                                                                                                                                                 50251 GCTTGGAGGGATATAAGATATAAGGAGACA 50221
                                                                                                                                                                                                                                                                                                                132 GTATAGATCTGGTAGCAAAGAAGAAGAACA 162
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray
TITLE OF INVENTION: Methods of Using the Sam
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
  Pred. No. 11;
0; Mismatches
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Pred. No. 1.
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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR PILING DATE: 2005-03-14
PRIOR PILING DATE: 2005-03-14
PRIOR PILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-03-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 214211, Application US/11266748A Publication No. US20060134663A1 GENERAL INFORMATION:
APPLICANT: Harkin, Paul
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Best Local Similarity 51.7%;
Matches 78; Conservative
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Best Local Similarity 53.3%;
Matches 73; Conservative
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; LOCATION: (869)..(869)
; OTHER INFORMATION: n is a,
US-11-266-748A-214211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JS-11-266-748A-214211/c
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Publication No. US20060286588A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: SAINZ, Jesus

TITLE OF INVENTION:

TITLE OF INVENTION: RISK OF TYPE 2 DIABETES MELLITUS

TITLE OF INVENTION: UNMER: US/11/454,296

CURRENT APPLICATION NUMBER: US/11/454,296

CURRENT APPLICATION NUMBER: US 60/692,174

PRIOR PILING DATE: 2006-06-16

PRIOR APPLICATION NUMBER: US 60/757,155

PRIOR APPLICATION NUMBER: US 60/757,155

SOFTWARE PERSONAL: 2006-01-06

NUMBER OF SEQ ID NOS: 53

SOFTWARE PARCHING DATE: 2006-01-06

NUMBER OF SEQ ID NOS: 53

SEQ ID NO 1

LENGTH:: 74930
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28 TCACTCAAGGGGCCAACCACAGCTGGGAGCCACTGCTCAGGGGAAGGTTCATATGGGACT
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                                                                                                   APPLICANT: GALLAIN, FALL
APPLICANT: Adhlaton, Patrick
APPLICANT: Adhlaton, Rarl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (19189)
CURRENT APPLICATION NUMBER: USO 11.03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
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PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2005-07-16
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Sequence 478637, Application US/11266748A Publication No. US20060134663A1
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SOFTWARE: PatentIn version 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 66.2'
Matches 51; Conservative
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US-11-266-748A-478637
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LENGTH: 715
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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-03-14
PRIOR PLILNG DATE: 2005-03-14
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LOCATION: (8834)..(8882)
OTHER INFORMATION: n = a, c, g, or t
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Best Local Similarity 53.3%;
Matches 73; Conservative
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LOCATION: (2001)..(2048)
OTHER INFORMATION: n = a,
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LOCATION: (6720)..(7498)
OTHER INFORMATION: n = a,
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; ORGANISM: Homo Sapiens
US-11-266-748A-129607
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              407 GGGCTGCTTTGCGAACAATGGCTGAGCATATAACCATAGGTTATGGGGAACAAAAC 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  623 GAATTCTTTAGTGTGGGTCTTAGGGCACTGCATCTCACACCAGCTGATGGGAACCATCTG 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                       Query Match 5.4%; Score 34.6; DB 8; Length 945; Best Local Similarity 53.3%; Pred. No. 1.1; Matches 73; Conservative 0; Mismatches 64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 129607, Application US/11266748A
Publication No. US20060134663A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: EP 04105479.2 PRIOR FILING DATE: 2004-11-03 PRIOR PELLING DATE: 2004-11-03 PRIOR FILING DATE: 2004-11-03 PRIOR APPLICATION NUMBER: EP 04105483.4 PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               467 AACATCAAAGTCACTGT 483
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; ORGANISM: Homo Sapiens
US-11-266-748A-76796
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US-11-266-748A-129607
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                                                                                   407 GGGCTGCTTTGGGAACAATGGCTGAGCATATAACCATAGGTTATGGGGAACAAAAC 466
                                                                                                     323 GAATTCTTTAGTGTGGGTCTTAGGGCACTGCATCTCACACCAGCTGATGGGAACCATCTG 382
                      Gaps
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Score 34.6; DB 8; Length 9 Pred. No. 1.1; 0; Mismatches 64; Indels
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| Sequence 46304, Application US/11056355B |
| Sequence 46304, Application US/11056355B |
| Publication No. US20060150283A1 |
| GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: Brover, Vyacheslav |
| APPLICANT: Brover, Vyacheslav |
| TILLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding |
| TILLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding |
| TILLE OF INVENTION: Polypeptides Encoded Thereby |
| FILE REFERENCE: 2750-1590PUS2 |
| CURRENT APPLICATION NUMBER: 60/544,190 |
| PRIOR APPLICATION NUMBER: 60/544,190 |
| PRIOR APPLICATION NUMBER: 60/544,190 |
| NUMBER OF SEQ ID NOS: 119966 |
| SEQ ID NO 46304 |
| LENGTH: 2704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 463 AAACAACATCAAAGTCACTGTATCAATTGCCATGAAGACTTGAGGGACCTGAATCTACCG 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                376 TAMAGICAGGAIGCCCAGGGGCCAGGGGGGGCTGCTTGGGAACAATGGCTGA
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LOCATION: (1)...(2704)
OTHER INFORMATION: Ortholog of Ceres SEQ ID NO 13582297
OTHER INFORMATION: as cited in SEQ ID NO 56486
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OTHER INFORMATION: Ortholog of Ceres SEQ ID NO 13586936
OTHER INFORMATION: as cited in SEQ ID NO 0
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Best Local Similarity 53.8%; Pred. No. 16;
Matches 71; Conservative 0; Mismatches
                                                                     NAME/KEY: misc_feature
LOCATION: (24443)..(24580)
OTHER INFORMATION: n = a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (28778)..(28871)
OTHER INFORMATION: n = a, c, g, or t
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ORGANISM: Arabidopsis thaliana
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LOCATION: (16167)..(16186)
OTHER INFORMATION: n = a,
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LOCATION: (1)..(2704)
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Sequence 35, Application US/11454296

Sequence 35, Application US/11454296

Publication No. US20060286588A1

GENERAL INFORMATION:

APPLICANT: GRAWT, SITUAN F. A.

TITLE OF INVENTION: GENETIC VARIANTS IN THE TCF7L2 GENE AS DIAGNOSTIC MARKERS FOR TITLE OF INVENTION: GENETIC VARIANTS IN THE TCF7L2 GENE AS DIAGNOSTIC MARKERS FOR TITLE OF INVENTION: GENETIC VARIANTS IN THE TCF7L2 GENE AS DIAGNOSTIC MARKERS FOR TITLE OF INVENTION NUMBER: US/11/454,296

CURRENT APPLICATION NUMBER: US 60/692,174

PRIOR FILING DATE: 2005-06-20

PRIOR FILING DATE: 2006-01-06

NUMBER OF SEQ ID NOS: 53

SOFTWARE: PATENTIN VERSION 3:3

SEQ ID NO 35

SEQ ID NO 35

SEQ ID NO 35
693 CTACACTCAAAAGCAACTTGACAACATCCAAGGAATTCACAGAAGCACCAGAAGCAGCGC 634
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   141 TAACATTAAGACAGTTTCACTCAGGAAACCAAACAGAACTTAGACACAATGCTTAGAAGC 82
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Pred. No. 2.2;
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                                                                                                                                                                                                                              AATGAAGAGCAGTACTTTAT 613
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; ORGANISM: Homo sapiens
US-11-454-296-35
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human, prostate cancer; diagnosis; tumour; gene therapy; detection; immunogenic; cytostatic; vaccine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polypeptide useful for treating and diagnosing prostate cancer comprises an immunogenic portion of prostate tumor protein.
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ABV27364
ABV27390
ABV22098
ABV25790
AAH93830
AAH93831
ACA59731
ACA59731
ACB5294
ACC95458
ADB14002
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ABV02479
ABV08703
AAZ95017
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AAD38826
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ABV11648
ABV11499
ABV41718
ABV41569
ABV27406
ABV27406
ABV27406
ABV27593
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98US-00116134.
98US-00159812.
99US-0023249.
99US-00232880.
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23-SEP-1998;
15-JAN-1999;
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09-APR-1999;
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immunogenic portion of a prostate tumour protein (PTP). The polypeptides and polymucleotides encoding them have cytostatic activity and can be used in vaccines and in gene therapy. The polypeptides and bolymucleotides encoding them, antigen presenting cells which express the polymeptides, antibodies against the polypeptides and vaccines comprising patient. The polypeptides are development of prostate cancer in a patient. The polypeptides can be used to generate antibodies or antibodies for passive immuno therapy. A portion of the modulate the expression of the polypeptides can be used as a probe or to modulate the expression of the polypeptides. AAAA6241 to AAA6691 and AAX82000 to AAX82000 represent sequences used in the exemplification of
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The present invention describes polymucleotide sequences (I) which encode prostate-specific proteins (II). (I) and (II) have cytostatic activity, and can be used in vaccine production and gene therapy. (I), (II), antibodies to (II), fusion proteins comprising (II), and isolated T cells prepared using (I) or (II) are used treat cancer in a patient. (I) and the antibodies are also used in the detection of cancer in a patient. The cancer that is diagnosed or treated is particularly prostate cancer. (I) and (II) can be used in vaccines. The antibodies or (I) can be used for monitoring the progression of cancer in a patient. (I) and (II) can also be used to improve diagnostic and therapeutic methods for prostate cancer. They can indicate the level of metastasis as well as the prostate polymucleotide and amino acid sequences used in the exemplification of
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                                                                                                                                                                                                                                                                                                                                                         New polynucleotide encoding a prostate-specific protein, for diagnosing, monitoring and treating prostate cancer in a patient and for use in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ACGATTTTCATTATCATGTAAAATCGGGTCACTCAAGGGGCCAACCACCACGGGGGAGCCAC
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Retter MW, Stolk JA, Skeiky YAW;
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           diagnosis; vaccine,
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100.0%; Pred. No. 6.6e-200;
tive 0; Mismatches 0;
          prostate-specific;
               Human, prostate cancer, prostate-specific
cytostatic, gene therapy, metastasis, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 324; 543pp; English.
                                                                                                                                                                                                                                                           Xu J, Dillon DC, Mitcham JL,
Kalos MD, Fanger GR, Day CH,
Wang A, Meagher MJ;
                                                                                                                                                           16-JAN-2001; 2001WO-US001574.
                                                                                                                                                                                            14-JAN-2000; 2000US-00483672
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Les 647; Conservative
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                                                               Homo sapiens
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300 360

Human prostate-specific cDNA sequence P712P.

(first entry)

04-OCT-2001

AAH93656;

AAH93656
ID AAH9
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AC AAH9
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DT 04-C
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DE HUME

AAH93656 standard; cDNA;

240

120

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protein, and for inhibiting the development of cancer especially prostate cancer. Compositions comprising the polymucleotide and/or polypeptide are useful for stimulating an immune response, and for treating cancer. The oligonucleotide is useful for detecting cancer. The prostate specific polymucleotide of the invention
                                                                    Sequence 647 BP; 190 A; 141 C; 154 G; 161 T; 0 U; 1 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human prostate-specific polypeptides and polynucleotides useful for diagnosis and treatment of cancer, especially prostate cancer.
               CATTTTGTGTGTGTGATAAAGTCAGGATGCCCAGGGGGCCCAGAGCAGGGGGGCTGCTTT
                                                           GGGAACAATGCTGAGCATATAACCATAGGTTATGGGGAACAAAACAACATCAAAGTCAC
                                                                                                        TGTATCAATTGCCATGAAGACTTGAGGGACCTGAATCTACCGATTCATCTTAAGGCAGCA
                                                                                                                                        GGACCAGTTTGAGTGGCAACAATGCAGCAGAATCAATGGAAACAACAGAATGATTGC
                                                                                           TGTATCAATTGCCATGAAGACTTGAGGGACCTGAATCTACCGATTCATCATAAGGCAGCA
                                                                                                                                                             GGACCAGITITGAGIGGCAACAATGCAGCAGCAGAATCAAIGGAAACAACAACAATGAITGC
  GGGAACAATGGCTGAGCATATAACCATAGGTTATGGGGAACAAAACAACATCAAAGTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention relates to isolated prostate-specific polynucleotides,
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Carter D;
                                                                                                                                                                                                                                                                                                                                                                     cancer; ss; cytostatic; immunostimulant; tumour.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 326; 579pp; English
                                                                                                                                                                                                                                                                                                                                            Human prostate cDNA sequence #301
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2000US-00568100.
2000US-00570737.
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2000US-00605783.
2000US-00636215.
2000US-00651236.
2000US-00657279.
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2000US-00685166
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09-AUG-2000;
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09-MAY-2000;
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  Length 647;
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                                            Indels
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100.0%; Score 646; DB 4; L
100.0%; Pred. No. 6.6e-200;
ive 0; Mismatches 0;
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                     Local Similarior
nes 647; Conservative
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The present invention describes an isolated polypeptide (P1) comprising at least an immunogenic portion of a prostate-specific protein, or its variant. Also described are polymucleotides (N1) encoding (P1). (P1) and (N1) have cytostatic activity and can be used in vaccine production. The polypeptides, nucleic acids and antibodies from the present invention are useful in the diagnosis and therapy of prostate cancer. Prostate specific genes P704P, P712P, P775P and B305D are located in a genomic region on chromosome 22q11.2 known as the Cat Bye Syndrome region.

Prostate specific antigen (PSA) P501S was located on chromosome 1.

AAH84671 to AAH85143 and AAG99000 to AAG99077 represent polynucleotide and polypeptide sequences used in the exemplification of the present
                   1 ACGATTTTCATTATCATGTAAAATGGGGTCACTCAAGGGGCCAACCACCACGGGGGAGGCCAC
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GGACCAGTTTGAGTGGCAACAATGCAGCAGCAGAATCAATGGAAACAACAGAATGATTGC
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Wang A;
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                                                                       Indels
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Skeiky YAW,
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100.0%; Pred. No. 6.6e-200;
ive 0; Mismatches 0;
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, Day CH,
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Kalos MD, Retter MW, Stolk JA,
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                                                                                                                                                                                                        AAH84970 standard; cDNA; 647
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                                                                                                                                                                                                                                                                                                                 The present invention describes an isolated polypeptide (I) comprising at least an immunogenic portion of a prostate tumour antigen protein or its variant. (I) have cytostatic activity and can be used in vaccine production. (I), prostate tumour antigen polynucleotides, an antigen presenting cell (APC e.g. a dendritic cell) that expresses (I), and a pharmaceutical composition containing (I) are useful for inhibiting the development of cancer in a patient. Antibodies specific for prostate specific proteins and oligonucleotides that hybridise to a polynucleotide that encodes a prostate specific protein are useful for detecting the presence or absence of a cancer or monitoring the progression of a cancer or monitoring the progression of a cancer, especially prostate cancer. AAH02422 to AAH2872, AAB7498 to AAB74821 and AAB74830 are sequences used in the
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                                          04-OCT-2000; 2000WO-US027464.
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The present invention describes compositions comprising peptides derived from the Wilm's tumour protein WT1 and methods for their use in treating malignant diseases. Peptides derived from both the murine and human WT1 proteins are provided. The human WT1 gene is found on chromosome 11p13, and the protein was shown to be a zinc finger transcription factor. The immunogenic peptides of the invention are particularly useful in the diagnosis and treatment of cancer and leukaemia. The present sequence is a coding sequence used in the exemplification of the invention
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                                                                                                                                                                                                                                                                                                                  Length 647;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           647
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                                                                                                                                                                                                                                                              647 BP; 190 A; 141 C; 154 G; 161 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                            6.6e-200;
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                                                                                                                                                                                                                                                                                                             Query Match
100.0%; Score 646; L
Best Local Similarity 100.0%; Pred. No. 6.6
Matches 647; Conservative 0; Mismatches
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CTAGAGAAAAGACCAACAACGGCCTCAAAGGATCTCTTACCATGAAGGTCTCAGCTAATT 300
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               TGCTCAGGGGAAGGTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAAA
                                                                                                                                     CCACCCCTCTGACCCTTTTGGAACTCCTCTGACCCTTTTAGAACAAGACTACCTAATATCTG
                                                                                                              cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
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97US-00904804.
98US-00030607.
98US-0015453.
98US-00159812.
99US-0023149.
99US-0028946.
99US-00439313.
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15.JAN-1999;
09.APR-1999;
13.JUL-1999;
12.NOV-1999;
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25-FEB-1998;
14-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention describes a fusion protein comprising at least one amino acid sequence of immunogenic portions of any of the 3 sequences not defined in the specification, or sequences having at least 70 or 90 % sequence identity to any one of the 35 sequences defined in the USPTO web site, which is encoded by any of the 4 nucleotide sequences not defined in the specification. The fusion protein, composition and methods are useful for diagnosing, preventing and/or treating cancer, particularly prostate cancer. The proteins are useful as markers to indicate the presence or absence of cancer. This sequence represents a prostate cancer therapy associated cDNs. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the US patent office at sequence. Last of the printed specification, but was obtained in electronic format unspto.gov/sequence.html?DocID=US20020192763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Prostate specific protein and its encoding polynucleotide, useful for the treatment and diagnosis of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
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prostatic acid phosphatase, PAP, prostate specific membrane antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kalos MD;
Carter D;
Hural J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 647 BP; 190 A; 141 C; 154 G; 161 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Fanger GR, Retteer MW, Stolk JA, Day CH, Vedvick TS, Li SX, Mang A, Skelky YAW, Hepler WT, Henderson RA, Mcneill PD, Houghton RL, Y De Bassolscv, Foy TW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 3; SEQ ID NO 308; 85pp; English.
                                                                                                                                                                                                                                                           04-OCT-1999; 99US-0157455P.
04-OCT-2000; 2000US-00679272.
28-MAR-2001; 2001US-00822827.
                                                                                                                                                                                                                   29-JUN-2001; 2001US-00895793.
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Y DE BASSOLS C V.
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Best Local Similarity 100.
Matches 647; Conservative
                                                                                                                                                                                                                                                                                                                                                                                   DILLON D C.
MITCHAM J L.
HARLOCKER S L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          JIANG Y.
KALOS M D.
FANGER G R.
STOLK J A.
DAY C H.
VEDVICK T S.
CARTER D.
LI S X.
WANG A.
SKEIKY Y A W.
HEPLER W T.
HENDERSON R A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MCNEILL P D.
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                         PSMA; gene; ss
                                                                      Homo sapiens.
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(HOUG/)
(DBAS/)
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(DILL/)
(MITC/)
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(JIAN/)
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(CART/)
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480

480 540 540 900 600

360 360 420 420

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240 240

540

us-09-232-880-308.rng

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The present invention relates to novel prostate-specific proteins (PSP) and their coding sequences. The PSPs and their coding sequences are useful for stimulating an immune response in a patient, or for treating prostate cancer in a patient and for determining, detecting or diagnosing the presence of a cancer in a patient. The present sequence was used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New prostate-specific proteins and genes, useful in gene therapy, particularly for stimulating an immune response in a patient, or treating prostate cancer in a patient, as well as for diagnosing prostate cancer
                                                                                                                                                                                                                                                                                            541 GGACCAGTTTGAGTGGCAACAATGCAGCAGAATCAATGGAAACAACAAGAATGATTGC
                          CTTGGCTAAGATGTGGGTTCCACATTAGGTTCTGAATATGGGGGGAAGGGTCAATTTGCT
                                                                                       CATTITICEGEGGGGGATAAAGTCAGGATGCCCAGGGGCCAGAGGGGGGCTGCTTTT
                                                                                                                                                                          GGGAACAATGGCTGAGCATATAACCATAGGTTATGGGGAACAAAACAACATCAAAGTCAC
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                                                                                                                                         GGGAACAATGGCTGAGCATATAACCATAGGTTATGGGGAACAAAACAACATCAAAGTCAC
                                                                                                                                                                                                                                                                           GGACCAGTTTGAGTGGCAACAATGCAGCAGCAGAATCAATGGAAACAACAGAATGATTGC
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Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS;
Li SX, Wang A, Skeiky YKW, Hepler WT, Hural J;
Houghton RL, Vinals Y pe BassolsC, Foy TM, Watanabe
                                                                                                                                                                                                                                                                                                                                              647
                                                                                                                                                                                                                                                                                                                                                                             647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cytostatic; gene therapy; prostate-specific protein; PSP; immune response; prostate cancer; 88.
                                                                                                                                                                                                                                                                                                                                              AATGECCTTTTTTTTCTCCTGCTTCTGACTTGATAAAGGGGACCGT
                                                                                                                                                                                                                                                                                                                                                             Prostate tumour specific cDNA sequence SEQ ID 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 3; Page 391-392; 691pp; English.
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29-JUN-2001; 2001US-00895814.
10-DEC-2001; 2001US-00012896.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACC95284 standard; cDNA; 647
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Mcneill PD,
Deng T;
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Carter D;
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diseases, in particular prostate cancer, and as markers for the
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100.0%; Pred. No. 6.6e-200;
ive 0; Mismatches 0;
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14.JAN-2000; 2000US-00483672.
09-MAY-2000; 2000US-0058857.
09-MAY-2000; 2000US-0058100.
12-MAY-2000; 2000US-00593737.
13-JUN-2000; 2000US-00593793.
27-JUN-2000; 2000US-0065783.
10-AUG-2000; 2000US-00651236.
06-SEP-2000; 2000US-00651236.
06-CT-2000; 2000US-00657279.
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Matches 647; Conservative
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WANG A.
SKEIKY Y A W.
HEPLER W T.
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MITCHAM J L.
HARLOCKER S I
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RETTER M W.
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DAY C H.
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KALOS M D.
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(KALO/)
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                                 Length 647;
               Sequence 647 BP; 190 A; 141 C; 154 G; 161 T; 0 U; 1 Other;
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                               Query Match
100.0%; Score 646; DB 8; L
Best Local Similarity 100.0%; Pred. No. 6.6e-200;
Matches 647; Conservative 0; Mismatches 0;
illustrate the invention
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Human; 88; prostate specific cDNA; cytostatic; immunostimulant; gene therapy; cell therapy; vaccine; T-cell epitope; class I major histocompatibility complex allele; MHC; prostate cancer; tumour; antigen presenting cell.
                                                                                                                                                             Human prostate specific cDNA P7112P.
ADB13758 standard; cDNA; 647 BP
                                                                                                      (first entry)
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ADB13758

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970S-00904804.
98US-00030607.
98US-00150607.
98US-00159812.
99US-00232149.
99US-00238946.
99US-00388946.
                                                                                                                                                         990S-00443686.
2000US-005368572
2000US-005368100.
2000US-00530137.
2000US-00537137.
2000US-00636215.
2000US-00636215.
2000US-00636215.
2000US-00636215.
2000US-00636216.
2000US-00636216.
2000US-00636216.
2000US-00636216.
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12-NOV-2002; 2002US-00294025
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09-FEB-2001;
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09-APR-1999;
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New isolated polypeptide for use in a vaccine for stimulating an immune response, or for treating or diagnosis cancer, preferably prostate

Example 3; Page; 101pp; English.

The invention relates to an isolated polypeptide comprising no more than 11-542 amino acids of ADB1353 comprising a sequence ADB1487. The peptides comprises a fragment ADB13563 of that contain naturally processed T-cell epitopes for 3 class I major histocompatibility complex (MHC) alleles. ADB13563 is a polypeptide encoded by a human prostate specific companion one of 68 disclosed as new. Also included are nucleic acids encoding the proteins and peptides expression vectors, a host cell transformed with the vector, an isolated antibody (or antigen binding cransformed with the vector, an isolated antibody (or antigen binding cransformed with the vector, an isolated antibody (or antigen binding cransformed with a binding agent that binds to the pretein or peptide, detecting the sample with a binding agent that binds to the peptides or a polypeptide cample with a binding agent that binds to the peptides or a polypeptide cample in a patient comparing the amount of polypeptide to a predetermine the presence of cancer), a fusion protein coff value to determine the presence of cancer), a fusion protein comprising the peptides or proteins, stimulating or eals that the peptides or proteins, stimulating or eals that the peptides or composition comprising the peptides, antibodies or composition comprising cells that express concer in a patient and treating prostate cancer in a patient and treating prostate cancer in a patient with the peptides or antigen presenting cells that express concer in a patient with the peptides or antigen presenting cells to the patient. The peptides (or an oligonucleotide that hybridises to nucleic acids encoding, or antigen-presenting cells expressing the nucleic acid, are used to antigen-presenting ells expressing the nucleic acid, are used to antigen-presenting cells repressing the nucleic acid, are used to antigen-presenting cells for the peptides.

US2003157089-A1

09-MAY-2002;

21-AUG-2003

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presenting cells are used to stimulate an immune response or treat prostate cancer in a patient. The present sequence is one of the disclosed human prostate specific CDNAs. Note: Except where otherwise indicated, the sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at sequence.
                                                                                                                                               1 ACGATITICATIATCATGIAAATCGGGTCACTCAAGGGGCCAACCACAGCTGGGAGCCAC
                                                                                                                                                                 TGCTCAGGGGAAGGTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAAA
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                                                                                                             Gaps
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                                                                                          Length 647;
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                                                                         Sequence 647 BP; 190 A; 141 C; 154 G; 161 T; 0 U; 1 Other;
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                                                                                          Score 646; DB 10;
Pred. No. 6.6e-200;
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                                                                                                           Mismatches
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Best Local Similarity 100.
Matches 647; Conservative
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27 MAR. 2000; 2000US-00536857. 09-MAY-2000; 2000US-00568100. 12-MAY-2000; 2000US-0057037. 13-JUN-2000; 2000US-00593793. 27-JUN-2000; 2000US-00605783. 09-AUG-2000; 2000US-00636215.

29-AUG-2000; 2000US-00651236. 06-SEP-2000; 2000US-00657279. 02-OCT-2000; 2000US-00659426. 10-OCT-2000; 2000US-00685166. 09-NOV-2000; 2000US-00709729.

12-JAN-2001; 2001US-00759143 09-FEB-2001; 2001US-00780669 09-MAY-2001; 2001US-00852911. 29-JUN-2001; 2001US-00895814 10-DEC-2001; 2001US-00012896

(CORI-) CORIXA CORP

99US-00439313. 99US-00443686. 2000US-00483672. 2000US-00536857.

14-JAN-2000;

13-JUL-1999; 12-NOV-1999; 18-NOV-1999;

970S-00904804. 980S-00020956. 980S-00115453. 980S-00159812. 990S-00232149. 990S-00352616.

14-JUL-1998; 23-SEP-1998; 15-JAN-1999; 09-APR-1999;

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.w polynucleotides encoding prostate specific polypeptides isolated
human prostate tumor cDNA library are useful to diagnose and treat
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                                               Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, H
Aralos MD, Franger GR, Retter MW, Stolk JA, Day CH, Ved
Carter D, Li SX, Wang A, Skelky YAW, Hepler WT, Hural
Mcneill PD, Houghton RL, Vinals Y De BassolsC, Foy TM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 647 BP; 190 A; 141 C; 154 G; 161 T; 0 U; 1 Other;
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100.0%; Pred. No. 6.6e-200;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                             cancer particularly prostate cancer
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                                                                                                                         Carter D, L
Mcneill PD,
Meagher MJ,
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100.0%; Pred. No. 6.6e-200;
tive 0; Mismatches 0;
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Matches 647; Conservative
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                                                     (CORI-) CORIXA CORP
                                                                     Dillon DC, N
MD, Fanger Gi
D, Li SX, V
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Kalos MD,
Carter D,
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TGCTCAGGGGAAGGTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAAA
                                    CCACCCCTCTGACCCTTTTGGAACTCCTCTGACCCTTTAGAACAAGCCTACTAATATCTG
                                                                                                           CCACCCCTCTGACCCCTTTGGAACTCCTCTGGACTCCTTTAGAACAAGCCTAATATCTG
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97US-00904804.
98US-00020607.
98US-0015912.
99US-00232149.
99US-00332149.
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01-AUG-1997;
09-FEB-1998;
25-FEB-1998;
14-JUL-1998;
23-SEP-1998;
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09-APR-1999;
13-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New fusion protein comprising a P501S polypeptide and an unrelated fu partner, useful for diagnosing, preventing, or treating cancer, such prostate cancer.
                                                                                                                                                                                                                                                                                                      Y, Reed SG;
Vedvick TS;
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                                                                                                                                                                                                                                                                                                      Jiang Y.
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GR, Retter MW, Stolk JA,
Wang A, Skeiky YAW;
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12-NOV-1999; 99US-00439313.
18-NOV-1999; 99US-00443686.
14-JAN-2000; 2000US-00483772.
27-MAR-2000; 2000US-00536857.
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541 GGACCAGTTTGAGTGGCAACAATGCAGCAGCAGAATCAATGGAAACAACAAAGAATGATTGC 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated polypeptide comprising no more than
                                                                                                                                                                                                                                                                                                                                                                                                                                             polypeptide for use in a vaccine for stimulating an immune for treating or diagnosis cancer, preferably prostate
                                                                                                           Human; 88; prostate specific cDNA; cytostatic; immunostimulant;
gene therapy; cell therapy; vaccine; T-cell epitope;
class I major histocompatibility complex allele; MHC; prostate cancer;
                                                                                                Human prostate antigen P712P additional DNA sequence.
                                                          ADB14484 standard; cDNA; 2577 BP
                                                                                                                                 tumour; antigen presenting cell.
                                                                                                                                                                                                       970S-00904804
980S-00020956
980S-00130607
980S-00159812
990S-00332149
990S-00352616
990S-0043568
2000US-0043686
2000US-004368572
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                                                                                                                                              Homo sapiens.
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09-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated
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                                                                                   18-DEC-2003
                                                                                                                                                                        02-OCT-2003
                                                                       ADB14484;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 6;
                                                                                                                                                                                                                                                                                                                                                                                                      (CORI-)
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                                            RESULT 13
                                                    ADB14484
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11-542 amino acida of ADB13563 comprising a sequence ADB14487. The peptides comprise a fragment ADB13563 of that contain naturally processed T-cell epitopes for 3 class I major histocompatibility complex (MHC) alleles. ADB13563 is a polypeptide encoded by a human prostate specific Tomba, one of 648 disclosed as new. Also included are nucleic acids concoling the proteins and peptides, expression vectors, a host cell tragment) that specifically binds to the protein or peptide detecting tragment) that specifically binds to the protein or peptide detecting the presence of a cancer in a patient (comprising contacting a patient campering the amount of polypeptide that binds to the protein or appearing as ADB1358, detecting the amount of polypeptide that binds to the agent and comparing the amount of polypeptides or a polypeptide appearing as ADB1358, detecting the amount of polypeptide that binds to the agent and comparising the presence of cancer), a tusion protein current comprising the peptides or proteins, stimulating or expanding T cells specific for a tumour protein comprising contacting T cells peptides or the solated T cell population, treating prostate cancer in a patient and treating prostate cancer in a patient and treating prostate cancer in a patient and treating prostate cancer in a patient and treating prostate cancer in a patient the T cells proliferate, and administering the peptides or antigen presenting cells to the patient. The peptides (or an oligonucleotide treating calls to the patient. The peptides (or an oligonucleotide cantigenes to nucleic acid encoding them), is used to detect the presence of cancer in a patient. The peptides, mucleic acids encoding, or stimulate or expand T cells specific for a tumour protein. The peptides, nucleic acids encoding the content protein apparent esequence similarity to one of the disclosed human prostate cancer in a patient. The present sequence is a known cDNA showing sequence similarity to one of the printed specification, the patient of the patient of the 
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Pred. No. 8e-185;
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98.1%;
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1 ACGATTTTCATTATCATGTAAATCGGGTCACTCAAGGGGCCAACCACCAGCTGGGAGCCAC
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2000US-0211314P.
2000US-021907P.
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pharmacogenomic marker;
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25-MAY-2000;
09-JUN-2000;
18-JUL-2000;
13-DEC-2000;
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                           The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV0010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; determining whether prostate cancer has metastasized in a patient; (i) assessing the aggressiveness or indolence of prostate cancer in a patient; (i) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                        GGACCAGTTTGAGTGGCAACAATGCAGCAGAATCAATGGAAACAACAGAATGATTGC 1231
                                                                                                                                                                                                                                                                                                   Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
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                                                                                                                 AATGICCTITITITICICCTGCTICIGACTIGATAAAGGG 641
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                                                                                                                                                                                                                                                                                Human prostate expression marker cDNA 21562
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                                                                                                                                                                                                       ABV21571 standard; cDNA; 1481
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16-MAR-2000; 2000US-01898G2P.
25-MAY-2000; 2000US-0207454P.
09-JUN-2000; 2000US-021314P.
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(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

Monahan JE Endege WO, Schlegel R,

WPI; 2001-662795/76

Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.

Claim 1; Page 3587; 11750pp; English

The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (d) assessing the aggressiveness or indolence of prostate cancer in a patient; (l) is also useful as a pharmacodyanamic or pharmacogenomic marker

Sequence 1481 BP; 364 A; 346 C; 314 G; 453 T; 0 U; 4 Other;

Gaps 4; Length 1481; Indels Score 599.2; DB 5; Pred. No. 2e-184; 0; Mismatches 9; Query Match 92.8%; Best Local Similarity 98.0%; Matches 628; Conservative

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AATGTCCTTTTTTTTCTCCTGCTTCTGACTTGATAAAAGGG 641 601

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501 AATGTCCTTTTTTTCTCCTCCTTCTGACTTGATAAAGGG 461

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AL512624 Human chr.
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CQ490122 Sequence
CQ495121 Sequence
CQ495511 Sequence
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CQ495513 Sequence
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AR60326 Sequence
AR610326 Sequence
AR768959 Sequence
AR563718 Sequence
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AR657118 Sequence
AR20922 Sequence
AR20925 Sequence
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CI2P21/08, CI2Q1/68, G01N33/574, G01N33/68//A61P35/00, C12N15/00,
A61K37/02,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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JIANGCHUN XU,
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Compounds for immunotherapy and diagnosis of prostate cancer and controls for their use.
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1 (lases 1 to 647)

11 (lases 1 to 647)

1110., D.C., Harlocker, S.L., Yuqiu, J., Xu, J. and Mitcham, J.L.

Compounds for immunotherapy and diagnosis of prostate cancer and methods for their use

Patent: JP 2002520054-A 300 09-JUL-2002;

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Location/Qualifiers
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PD 09-JUL-2002
PF 14-JUL-1999 JP 2000560247
PR 14-JUL-1999 US 09/115453,
23-SEP-1999 US 09/222880,15-JA
09-APR-1999 US 09/22880,15-JA
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AY338953
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CQ48960
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JP 2002520054-A/300.
Homo sapiens (human)
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AR278420 Sequence
AR371012 Sequence
AR40152 Sequence
AR405419 Sequence
AR405419 Sequence
AR53799 Sequence
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Xa,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Diang,Y.,

Xalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,

Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,

Hepler,W.T. and Henderson,R.A.

Compositions and methods for the therapy and diagnosis of prostate
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Xu,J., Dillon,D.C. and Mitcham,J.L.
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Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L. and Yuqiu,J. Prostate specific fusion protein compositions
Patent: US 6395278-A 308 28-MAY-2002;
Corixa Corporation; Seattle, WA
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/organism="unknown"
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Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Yuqiu,J.,
Reed,S.G., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A. and
Day,C.H.
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Corixa Corporation; Seattle, WA
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1 (Carter, Mitcham, J.L., Harlocker, S.L., Jiang, Y., Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H., Vedvick, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A.W., Hepler, W.T. and Henderson, R.A.
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Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skelky,Y.A.W.,
Hepler,W.T. and Henderson,R.A.

Compositions and methods for the therapy and diagnosis of prostate
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; Score 646; DB 2; I
; Pred. No. 7.6e-202;
0; Mismatches 0;
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US 6630305.
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Corixa Corporation; Seattle,
WOX;
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/organism="unknown"
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Sequence 308 from patent
AR405419
AR405419.1 GI:40154256
   Query Match
Best Local Similarity 100.0%;
Matches 647; Conservative 0
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Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H., Vedvick,T.S., Carter,D., S.X., Wang,A., Skelky,Y.A.W., Hepler,W.T. and Henderson,R.A.
Compositions and methods for the therapy and diagnosis of p
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Corixa Corporation; Seattle, WA
Location/Qualifiers
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ARS63799
ARS63799.1 GI:53978850
                                                  0; Mismatches
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                                                                                                      AGGATTTTCATTATCATGTAAAATCGGGTCACTCAAGGGGCCAACCACGAGCTGGGAGCCAC
                                                                                                                                          TGCTCAGGGGAAGGTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGTATATAAA
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                                   Query Match 100.0%; Score 646; DB 2; L. Best Local Similarity 100.0%; Pred. No. 7.6e-202; Matches 647; Conservative 0; Mismatches 0;
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1 (bases I to 647)

Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y.,
Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H.,
Vedvick, T.S., Carter, D., Li, S.X., Wang, A., Skelky, Y.A.W.,
Hepler, W.T. and Henderson, R.A.
Compositions and methods for the therapy and diagnosis of prostate
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Corixa Corporation; Seattle, WA
Location/Qualifiers
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/organism="unknown"
/wol_type="genomic DNA"
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Sequence 308 from patent
AR605605
AR605605.1 GI:56657269
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Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Diang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,
Hepler,W.T. and Henderson,R.A.
Compositions and methods for the therapy and diagnosis of prostate
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Corixa Corporation; Seattle, WA
Location/Qualifiers
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   'mol_type="genomic DNA
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Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jay,C.H.,
Kalos,M.D., Fanger,G.R., Retter,M., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Mang,A., Skeiky,Y.A.W.,
Hepler,W.T., Henderson,R.A., Hural,J., McNeill,P.D., Houghton,R.L.,
Vinals y de Bassols,C., Foy,T.M., Watanabe,Y. and Meagher,M.J.
Compositions and methods for the therapy and diagnosis of prostate
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Patent: US 6894146-A 308 17-MAY-2005;
Corixa Corporation; Seattle, WA
                /organism="unknown"
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGGAACAATGGCTGAGCATATAACCATAGGTTATGGGGAACAAAAACAACATCAAAGTCAC
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                                                                                                                                                                                                                            100.0%; Score 646; DB 2; L
ilarity 100.0%; Pred. No. 7.6e-202;
Conservative 0; Mismatches 0;
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CORIXA CORPORATION (US)
Location/Qualifiers
1. .647
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/ the trace of the trace of the trace of the trace of the trace of the trace of the trace of the trace of the trace of the trace of the trace of the trace of the trace of the trace of the trace of the trace of the trace of the trace of the trace of the trace of the trace of the trace of the trace of trace of the trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of trace of 
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Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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    Patent: US 6943236-A 308 13-SEP-2005;
Corixa Corporation; Seattle, WA
Location/Qualifiers
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                                                                       1. .647
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Compositions and methods for therapy and diagnosis of prostate
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               cancer Patent: WO 0125272-A 308 12-APR-2001, CORIXA CORPORATION (US)
                                                                                       1. .647
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1. .647
/note="n = A,T,C or G"
                                                                                                                                                                 misc_feature
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Search completed: December 31, 2006, 18:35:31 Job time : 4169.51 secs

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| FMC_Celerra_SIDS3/ptodata/2/ina/6_COMB.seq:*
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| FMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
| FMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
| FMC_Celerra_SIDS3/ptodata/2/ina/PE_COMB.seq:*
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Listing first 45 summaries
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Sequence 12702, A	Sequence 14, Appl	Sequence 2464, Ap	Sequence 5097, Ap	Sequence 639, App	Sequence 717, App	Sequence 16664, A	Sequence 2463, Ap	Sequence 5096, Ap	Sequence 196408,	Sequence 12896, A	Sequence 17305, A	Sequence 1739, Ap	Sequence 2436, Ap	Sequence 250, App	Sequence 97, Appl	Sequence 481, App	Sequence 1, Appli	Sequence 17612, A	Sequence 12427, A	Sequence 13438, A	Sequence 13379, A
US-09-513-999C-12702	US-08-232-463-14	US-09-949-002-2464	US-09-949-002-5097	US-09-949-002-639	US-09-949-002-717	US-09-949-016-16664	US-09-949-002-2463	US-09-949-002-5096	US-09-949-016-196408	US-09-949-016-12896	US-09-949-016-17305	US-09-583-110-1739	US-09-107-433-2436	US-09-769-787-250	US-08-961-527-97	US-09-490-609B-481	US-10-262-083-1	US-09-949-016-17612	US-09-949-016-12427	US-09-949-016-13438	US-09-949-016-13379
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44.6	43	34.8	34.8	34.8	34.8	34.8	34.4	34.4	34.2	34.2	34.2	34	34	33.4	33.4	32.6	32.6	32.6	32.6	32.6	32.4
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ALIGNMENTS

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TGCTCAGGGGAAGGTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAAA 120
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APPLICANT: Jiang Yuqui
APPLICANT: Alang Yuqui
APPLICANT: Ralos, Michael
APPLICANT: Reded, Steven G.
APPLICANT: Reter, Mark
APPLICANT: Reter, Mark
APPLICANT: Reter, Mark
APPLICANT: Banger, Gary
APPLICANT: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: COMPOSITIONS OF PROSITE CANCER
TITLE OF INVENTION: DIAGNOSIS OF PROSITE CANCER
TITLE SEPERBUCE: 21012.42709;
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT APPLICATION NUMBER: US/09/439,313
SOPTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 308
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RESUL. 1
US-09-439-313-308
; Sequence 308, Application US/09439313
; Patent No. 6129505
; GENERAL INFORMATION:
; APPLICANT: W, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Cennifer L.
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; OTHER INFORMATION: n = A, T, C or G
US-09-439-313-308
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ORGANISM: Homo sapien
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                                                   GGACCAGTTTGAGTGCCAACAATGCAGCAGCAGAATCAATGGAAACAACAGAATGATTGC
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US-09-232-149A-308

JOS-232-149A-308

Sequence 308, Application US/09232149A

Patent No. 6465611

GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121-427C6
CURRENT PILICATION NUMBER: US/09/232,149A

CURRENT FILING DATE: 1999-01-15

NUMBER OF SEQ ID NOS: 338

SOFTWARES: FastSEQ for Windows Version 3.0

SEQ ID NO 308

LENGTH: 647
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100.0%; Score 646; DB 3; L
Best Local Similarity 100.0%; Pred. No. 2.1e-206;
Matches 647; Conservative 0; Mismatches 0;
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j OTHER INFORMATION: n = A,T,C or G
US-09-232-149A-308
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GENERAL INFORMATION:
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Jang, Yugui
APPLICANT: Alarlocker, Susan Louise
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOUNS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
CURRENT APPLICATION UNDBER: 19599/352,616A
CURRENT RILING DATE: 1999-07-13
NUMBER OF SEQ ID NOS: 472

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 308
LENGTH: 647
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 2
US-09-352-616A-308
Sequence 308, Application US/09352616A
; Patent No. 6395278
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OTHER INFORMATION: n = A,T,C or G
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ORGANISM: Homo sapien
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100.0%; Pred. No. 2.1e-206;
ive 0; Mismatches 0;
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US-09-685-166A-308
; Sequence 308, Application US/09685166A
; Patent No. 6630305
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GENERAL INPORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Dennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Henderson, Robert A.
APPLICANT: Fanger, Rach
APPLICANT: Ralos, Michael D.
APPLICANT: Ralos, Michael D.
APPLICANT: Rolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Carter, Marc W.
APPLICANT: Carter, Marc W.
APPLICANT: Carter, Dayr Craig H.
                                             = A,T,C or
                                                                                       Query Match
Best Local Similarity 100.
Matches 647; Conservative
; FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(647)
CTHER INFORMATION: n =
US-09-636-215-308
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                                             CATTITICIGIGGATAAAGTCAGGATGCCCAGGGGCCAGAGCAGGGGGCCTGCTTTT
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APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.42717C17
CURRENT APPLICATION NUMBER: US/09/636,215
CURRENT FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 852
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 308
LENGTH: 647
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Patent No. 6620922
GENERAL INFORMATION:
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Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
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Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
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Vedvick, Thomas
Carter, Darrick
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ORGANISM: Homo sapien
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NAME/KEY: misc feature
LOCATION: (1)...(647)
COTHER INFORMATION: n = A,T,C or
US-09-688-489-308
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Best Local Similarity 100.
Matches 647; Conservative
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APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
TITLEONI: William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REPERENCE: 210121.427C21
CURRENT APPLICATION NUMBER: US/09/685,166A
CURRENT FILING DATE: 2000-10-10
NUMBER OF SEQ ID NOS: 898
SOFTWARE: PESESEQ for Windows Version 3.0
SEQ ID NO 308
LENGTH: 647
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LOCATION: (1)...(647)
OTHER INFORMATION: n = A,T,C or
                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapien
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: M, Jiangchun

APPLICANT: Dillon, Davin C.

APPLICANT: Mitcham, Jennifer Lynn

APPLICANT: Mitcham, Jennifer Lynn

TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE

TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE

TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE

CURRENT APPLICATION NUMBER: US/09/688,489

CURRENT FILING DATE: 2000-10-13

NUMBER OF SEQ ID NOS: 338

SOFTWARE: FastSEQ for Windows Version 3.0

LENGTH: 647
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RESULT 7 US-09-679-426-308

RESULT 6 US-09-688-489-308 ; Sequence 308, Application US/09688489

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TGTATCAATTGCCATGAAGACTTGAGGGACCTGAATCTACCGATTCATCTTAAGGCAGCA
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Patent No. 6800746
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; OTHER INFORMATION: n = A,T,C or G
US-09-759-143-308
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Harlocker, Susan L.
Jiang, Yuqui,
Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
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Skeiky, Yasir A.W.
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Vedvick, Thomas S.
Carter, Darrick
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Dillon, Davin C.
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Best Local Similarity 100.
Matches 647; Conservative
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ORGANISM: Homo sapien
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CURRENT APPLICATION NUMBER: US/09/679,426

CURRENT FILING DATE: 2000-10-02

NUMBER OF SEQ ID NOS: 895
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100.0%; Score 646; DB 3; Length 647;
Best Local Similarity 100.0%; Pred. No. 2.16-206;
Matches 647; Conservative 0; Mismatches 0; Indels
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Application US/09679426
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LOCATION: (1)...(647)
OTHER INFORMATION: n = A,T,C or G
                                         Xu, Jiangchun
Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
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Wang, Aijun
Skeiky, Yasir A.W.
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Vedvick, Thomas
Carter, Darrick
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Retter, Marc W.
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                                                                                                                                                                                  John A.
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ORGANISM: Homo sapien
              Patent No. 6759515
GENERAL INFORMATION:
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LENGTH: 647
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE STREEFERNCE: 210121.47C23
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
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100.0%; Pred. No. 2.1e-206;
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1 ACGATTTTCATTATCATGTAAATCGGGTCACTCAAGGGGCCCAACCACCAGCTGGGAGCCAC
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; Patent No. 6894146
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APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Henderson, Robert A.
APPLICANT: Ralos, Michael D.
APPLICANT: Ralos, Michael D.
APPLICANT: Ralos, Michael D.
APPLICANT: Ralos, Michael D.
APPLICANT: Ralos, Michael D.
APPLICANT: Ralos, John A.
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Vedvick, Thomas S.
Carter, Darrick
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US-09-657-279-308
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 GGGAACAATGGCTGAGCATATAACCATAGGTTATGGGGAACAAAACAACAACTAAGTCAC
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APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yaair A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: OONGOSIS OF PROSTATE CANCER
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
CURRENT PELING DATE: 2000-08-29
NUMBER OF SEQ ID NOS: 865
SOFTWARE FALSEQ for Windows Version 3.0
SEQ ID NO 308
LENGTH: 647
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100.0%; Score 646; DB 3; Length 647;
Best Local Similarity 100.0%; Pred. No. 2.1e-206;
Matches 647; Conservative 0; Mismatches 0; Indels
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Henderson, Robert A.
Kalos, Michael D.
Ranger, Gary R.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
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Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
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NAME/KEY: misc_feature
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ORGANISM: Homo sapien
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US-09-651-236-308
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US-09-651-236-308
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GGGBACAATGCTGAGCATATAACCATAGGTTATGGGBACAAAACAACATCAAAGTCAC 480 CTAGAGABAAAGGACCAACAACAACGGCCTCAAAGGATCTCTTACCATGAAGGTCTCAGCTAATT 300 361 CATTITIGLGIGGATAAAGTCAGGATGCCCAGGGGCCAGGGCAGGGGCTGCTTT 420 421 gegaacaaregereaageararaacearaegerraregegaacaaacaacarcaaagreac 480 TGCTCAGGGGAAGGTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAAA 120 CTTGGCTAAGATGTGGGTTCCACATTAGGTTCTGAATATGGGGGGAAGGGTCAATTTGCT CTAGAGAAAAGACCAACAACGCCTCAAAGGATCTCTTACCATGAAGGTCTCAGCTAATT CTTGGCTAAGATGTGGGTTCCACATTAGGTTCTGAATATGGGGGGGAGGGTCAATTTGCT GGACCAGTTTGAGTGGCAACAATGCAGCAGCAGAATCAATGGAAACAACAGAATGATTGC TGTATCAATTGCCATGAAGACTTGAGGGACCTGAATCTACCGATTCATCTTAAGGCAGCA CATTITGIGIGGATAAAGTCAGGATGCCCAGGGGCCAGAGCAGGGGGCTGCTTTT APPLICANT: Skeiky, Yaair A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121-427C19
CURRENT APPLICATION NUMBER: US/09/657,279
CURRENT FILING DATE: 2000-09-06
NUMBER OF SEQ ID NOS: 877
SOFTWARE: FastsEQ for Windows Version 3.0 647 647 601 AATGTCCTTTTTTTTCTCCTGCTTCTGACTTGATAAAAGGGGACCGT AATGTCCTTTTTTTTTTTCTCCTGCTTCTGACTTGATAAAAGGGGACCGT

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61 TGCTCAGGGGAAGGTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAAA 120
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APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Gary R.
APPLICANT: Mantanabe, Yoshihiro
APPLICANT: Madaleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.47727
CURRENT APPLICATION NUMBER: US/10/012,896
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 308
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100.0%; Pred. No. 2.1e-206;
tive 0; Mismatches 0;
                                                                                 Hural, John
McNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
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                               Skeľky, Ýasir A.W.
Hepler, William T.
Henderson, Robert A.
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Best Local Similarity 100.
Matches 647; Conservative
                   Wang, Aijun
                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Homo sapiens
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Patent No. 6943236
GENERAL INFORMATION:
APPLICANT: XU, Jiangchun
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Vedvick, Thomas S.
                                                                   ; LOCATION: (1)...(647)
; OTHER INFORMATION: n = A,T,C or US-09-657-279-308
                                                 NAME/KEY: misc_feature
LOCATION: (1)...(647)
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
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Best Local Similarity
Matches 647; Conserv
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US-10-012-896-308
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                                                                    CTTGGCTAAGATGTGGGTTCCACATTAGGTTCTGAATATGGGGGGAAGGGTCAATTTGCT
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Pred. No. 2.6e-190;
0; Mismatches 9;
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Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
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Dillon, Davin C.
Mitcham, Jennifer L.
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98.0%;
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Best Local Similarity 98.0
Matches 628; Conservative
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US-09-636-215-552
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APPLICANT: FOY, Teres M.
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Deng, Ta
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C28
CURRENT FILING DATE: 2002-08-12
NUMBER OF SEQ ID NOS: 1033
SOFTWARE: FASELSEQ for Windows Version 3.0
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                                                       100.0%; Score 646; DB 5; Length 647; 100.0%; Pred. No. 2.1e-206; Live 0; Mismatches 0; Indels
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US-10-144-678A-308
; Sequence 308, Application US/10144678A
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NAME/KEY: misc_feature
LOCATION: 123
OTHER INFORMATION: n = A,T,C or G
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McNeill, Patricia D.
Houghton, Raymond L.
Vinals y de Bassols, C:
Poy, Teresa M.
Watanabe, Yoshihiro
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Ranger, Gary R.
APPLICANT: Fanger, Gary R.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
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Hepler, William T.
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Matches 647; Conservative
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ORGANISM: Homo sapiens
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Li, Samue]
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Best Local Similarity
Matches 628; Conserv
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    US-09-685-166A-552
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CTAGAGAAAAGACCAACAGCCTCAAAGGATCTCTTACCATGAAGGTCTCAGCTAATT 300
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                                                               APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Renger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Usy, Carig H.
APPLICANT: Usy, Samuel
APPLICANT: Li, Samuel
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky Sasir A.W.
APPLICANT: Sasir A.W.
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ORGANISM: Homo sapiens
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1112 IGTATCAATIGCCAIGAAGACICGAGGGACCIGAAICTACGAITCAICTTAAGGCAGCA 1171
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Score 599.2; DB 3;
Pred. No. 2.6e-190;
0; Mismatches 9;
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Patent No. 6759515
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Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
92.8%;
98.0%;
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Skeiky, Yasir A.<sup>1</sup>
Hepler, William
                                   Conservative
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER FILE REFERENCE: 210121.427C20
CURRENT APPLICATION NUMBER: US09/679,426
CURRENT FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 895
SOFTWARE: FASTSEQ FOR Windows Version 3.0
LENGTH: 2577
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                                                                                                                TYPE: DNA
CORGANISM: Homo sapiens
US-09-679-426-552
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GenCore version 5.1.9
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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US-09-439-131-474
US-09-685-166A-474
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US-09-671-236-474
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US-09-439-313-311

US-09-439-313-311

Sequence 311, Application US/09439313

Patent No. 6329505

GENERAL INFORMATION:
APPLICANT: Micham, Davin C.
APPLICANT: Micham, Davin C.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Ranger, Gary
APPLICANT: Read, Steven G.
APPLICANT: Read, Steven G.
APPLICANT: Read, Steven G.
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APPLICANT: Applicant: Name and Applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant applicant a
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100.0%; Pred. No. 9.5e-125;
ive 0; Mismatches 0;
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OTHER INFORMATION: n = A,T,C or G
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ORGANISM: Homo sapien
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                                                  TCTCTTTACAGGGAGCTCCTGCAGCCCCTACAGAAATGAGTGGCTGAGATTCTTGATTGC 420
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; Sequence 311, Application US/09232149A
; Patent No. 6465611
; GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
; TITLE OF INVENTION: 1999-01-15
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE PASSEQ for Windows Version 3.0
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US-09-232-149A-311
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ORGANISM: Homo sapien
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LENGTH: 526
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; Patent No. 6395278
; Batent No. 6395278
; Batent No. 6395278
; Batent No. 6395278
; BAPLICANT: Harlocker, Susan Louise
APPLICANT: Harlocker, Susan Louise
APPLICANT: W. Jiang, Yuqui
APPLICANT: W. Jiangchun
TITLE OF INVENTION: OP PROSTATE CANCER AND METHODS FOR THEIR USE
TITLE OF INVENTION: OP PROSTATE CANCER AND METHODS FOR THEIR USE
CURRENT APPLICATION NUMBER: US/99/352,616A
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 311
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OTHER INFORMATION: n = A, T, C or
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NAME/KEY: misc_feature
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ORGANISM: Homo sapien
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US-09-352-616A-311
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  181 ATTAAACATGGAATAAAGATTTGTCCTTAAATATAATCTACAAGAAGACTTTGATATTTG 240
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                                                                                                                        301 AAAATGGGGAAACTCTGAAGGGTTTTAAGTATCTTACCTGAAGCTACAGACTCCATAACC
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                                        241 TTTTTCACAAGTGAAGCATTCTTATAAAGTGTCATAACCT
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APPLICANT: Skeiky, Wasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ITITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 210121.427C21
CURRENT APPLICATION NUMBER: US/09/685,166A
CURRENT FILING DATE: 2000-10-10
WUMBER OF SEQ ID NOS: 898
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 311
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GENERAL INFORMATION:
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NAME/KEY: misc feature

LOCATION: (1)...(526)

OTHER INFORMATION: n = A,T,C or G
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Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
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Vedvick, Thomas S
Carter, Darrick
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Best Local Similarity
Matches 526; Conserval
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US-09-685-166A-311
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Gaps
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CURRENT FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 852
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Patent No. 6620922
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; OTHER INFORMATION: n = A,T,C or G
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Mitcham, Jennifer L.
Harlocker, Susan L.
Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
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Skeiky, Yasır A.W.
Hepler, William
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Vedvick, Thomas S
Carter, Darrick
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Retter, Marc W.
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Patent No. 6664377

GENERAL INPORMATION:
APPLICANT: Wi Jiangchun
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR THEIR USE
TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.42702
CURRENT FILING DATE: 2000-10-13

NUMBER OF SEQ ID NOS: 338

SOFTWARE: FastSEQ for Windows Version 3.0

LENGTH: 526
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| LOCATION: (1)...(526)
| OTHER INFORMATION: n = A,T,C or G
US-09-688-489-311
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Best Local Similarity
Matches 526; Conserv
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                                                                                        CATTTACAGCATTTAAAATGTGTTCAGCATGAAATATTAGCTACAGGGGAAGCTAAAATAA 180
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  1 CAAATTTGAGCCAATGACATAGAATTTTTACAAAATCAAGAAGCTTATTCTGGGGCCATTTC
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REPERENCE: 21012.42718C18
CURRENT APPLICATION NUMBER: US/09/651,236
CURRENT FILING DATE: 2000-08-29
NUMBER OF SEQ ID NOS: 865
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Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
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Dillon, Davin C.
Mitcham, Jennifer L.
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Vedvick, Thomas S.
Carter, Darrick
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ORGANISM: Homo sapien
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APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlock Michael D.
APPLICANT: Ranger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Carter, Dohn A.
APPLICANT: Octorer, Darrick
APPLICANT: Usamuel
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: OCHOROSITIONS AND METHODS FOR THE THERAPY AND
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CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSEQ for Windows Version 3.0
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; OTHER INFORMATION: n = A,T,C or
US-09-759-143-311
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ORGANISM: Homo sapien
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; SEQ ID NO 311
; LENGTH: 526
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KRY: misc feature
; LOCATION: (1)...(526)
; OTHER INFORMATION: n = A US-09-657-279-311
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US-10-012-896-311
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                                                                                                       1 CAAATTTGAGCCAATGACATAGAATTTTACAAATCAAGAAGCTTATTCTGGGGGCCATTTC
                                                                                                                      CATTTACAGCATTTAAAATGTGTTCAGCATGAAATATTAGCTACAGGGGAAGCTAAATAA
                                                                                                                                                                                                                                                                                ATTAAAACATGGAATAAAAGATTTGTCCTTAAAATATAAATCTACAAGAAGACTTTGATATTTG
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                                                                          Gaps
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APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427019
CURRENT APPLICATION NUMBER: US/09/657,279
CURRENT APPLICATION NUMBER: 05/00-09-06
NUMBER OF SEQ ID NOS: 877
SOFTWARE: FASESEQ FOR WINDOWS Version 3.0
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tive 0; Mismatches 0;
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Patent No. 6894146
PAPERAL INFORMATION:
APPLICANT: Xu, Jiangchun
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Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
     = A,T,C or
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Best Local Similarity 100.C
Matches 526; Conservative
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Wang, Aijun
       OTHER INFORMATION: n
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US-09-657-279-311
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100.0%; Score 525; DB 3; L
Best Local Similarity 100.0%; Pred. No. 9.5e-125;
Matches 526; Conservative 0; Mismatches 0;
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APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Kalos, Michael D.
APPLICANT: Stols, More W.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Carter, Marc W.
APPLICANT: Carter, Marc W.
APPLICANT: Li, Samuel X.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aljun
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Skeiky, Yasir A.W.
Hepler, William T.
Henderson, Robert A.
Hural, John
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Vinals y de Bassols,
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Watanabe, Yoshihiro
  Harlocker, Susan L.
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Hepler, William T.
                      Jiang, Yuqiu
Henderson, Robert
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Carter, Darrick
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Best Local Similarity 100.
Matches 526; Conservative
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ORGANISM: Homo sapiens
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                                                                               APPLICANT: Fanger, Gary R.
APPLICANT: Wanterande, Yoshihiro
APPLICANT: Wanterande, Yoshihiro
APPLICANT: Wanterande, Yoshihiro
APPLICANT: Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
CURRENT EPFERENCE: 210121.427C27
CURRENT APPLICATION NUMBER: US/10/012,896
NUMBER OF SEQ ID MOS: 1011
SOFTWARE: FastSEQ for Windows Version 3.0
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Best Local Similarity 100.0%; Pred. No. 9.5e-125;
Matches 526; Conservative 0; Mismatches 0;
                   Houghton, Raymond L.
Vinals de Bassols, Carlota
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OTHER INFORMATION: n = A,T,C or G
McNeill, Patricia D.
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ORGANISM: Homo sapiens
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APPLICANT: Deng, Ta
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C28
CURRENT APPLICATION UNDBER: US/10/144,678A
CURRENT FILING DATE: 2002-08-12
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100.0%; Pred. No. 9.5e-125;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 3434;
526
                                                                                                                                                                                                                                                                                                                      APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                481 AGTTCTATAAACTGTAGTNTACTTATTTTAATCCCCAAAGCACAGT
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Pred. No. 2.9e-110;
0; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1959-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: PASESEQ for Windows Version 3.0
                                                                                                                                                        APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Jiang Yuqui
APPLICANT: Reed, Steven G.
APPLICANT: Kalos, Michael
APPLICANT: Fanger, Gary
APPLICANT: Setter, Mark
APPLICANT: Solk, John
APPLICANT: Day, Craig
                                                                                                           Sequence 476, Application US/09439313
Patent No. 6329505
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 97.9%;
Matches 507; Conservative
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ORGANISM: Homo sapiens
                                                                                RESULT 13
US-09-439-313-476/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 476
LENGTH: 3434
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121 CATTTACAGCATTTAAAATGTGTTCAGCATGAAATATTAGCTACAGGGGAAGCTAAATAA 180
1942 CATTTACAGCATTTAAAATGTGTTCAGCATGAAATATTAGCTACAGGGAAAGCTAAATAA 2883
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Complex, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REPERENCE: 210121.42717C17
CURRENT PRILING DATE: 2000.08-10
NUMBER OF SEQ ID NOS: 852
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2584 AGTTCTATAAACTGTAGT-TACTTATTTTAATCCCAAA 2548
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                                                                                                                                   , Sequence 476, Application US/09636215; Patent No. 6620922
                                                                                                                                                                                                                         Xu, Jiangchun
Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
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Henderson, Robert A.
Kalos, Michael D.
Fenger, Gary R.
Retter, Marc W.
Stolk, John A.
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Vedvick, Thomas S.
Carter, Darrick
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Matches 507; Conservative
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                  ; GENERAL INFORMATION:
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APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C21
CURRENT APPLICATION NUMBER: US/09/685,166A
CURRENT APPLICATION NUMBER: US/09/685,166A
SURRENT FILING DATE: 2000-10-10
NUMBER OF SEQ ID NOS: 898
SOFTWARE: FASELSEQ for Windows Version 3.0
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                       481 AGTICTATAAACTGTAGINTACTIATITAATCCCCAA 518
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                                                                                                        RESULT 15
US-09-685-166A-476/c
Sequence 476, Application US/09685166A
Pacent No. 6630305
GENERAL INFORMATION:
                                                                                                                                                                                                                   APPLICANT: Xu. Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Dayrick
APPLICANT: Carter, Dayrick
APPLICANT: Carter, Dayrick
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CORGANISM: Homo sapiens
US-09-685-166A-476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 476
LENGTH: 3434
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APPLICANT:
APPLICANT:
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Result		Query				
No.	Score	Match	Match Length DB	DB	ID	Description
7	525	100.0	526	m	AAA06543	Aaa06543 Human imm
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m	525	100.0	526	4	AAS63752	Aas63752 Human pro
4	525	100.0	526	4	AAH02724	Aah02724 Prostate
S	525	100.0	526	4	AAH84973	Aah84973 Human pro
9	525	100.0	526	4	AAF86941	Aaf86941 Human P77
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60	525	100.0	526	9	ABL95123	Ab195123 Human P77
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10	525	100.0	526	10	ADB13761	Adb13761 Human pro
11	525	100.0	526	2	ADG26177	Adg26177 Human pro
12	525	100.0	526	15	AEF66458	Aef66458 Human pro
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16	477.2	90.9	1203	Ŋ	ABV21774	Abv21774 Human pro
17	469.2	89.4	634	Ŋ	ABV43033	Abv43033 Human pro
c 18	469.2	89.4	3434	4	AAH93811	Aah93811 Human pro

The present invention describes isolated polypeptides, comprising an

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19-JUL-2001

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immunogenic portion of a prostate tumour protein (PTP). The polypeptides and polynucleotides encoding them have cytostatic activity and can be used in vaccines and in gene therapy. The polypeptides and polynucleotides encoding them, antigen presenting cells which express the polypeptides, antibodies against the polypeptides and vaccines comprising them can be used for inhibiting the development of prostate cancer in a patient. The polypeptides can be used to generate antibodies or antidiotypic antibodies for passive immuno therapy. A portion of the polynucleotides encoding the polypeptides can be used as a probe or to modulate the expression of the polypeptides. AAA06241 to AAA08691 and AAY82000 to AAY82020 represent sequences used in the exemplification of the present invention
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The present invention describes polynucleotide sequences (I) which encode prostate—specific proteins (II). (I) and (II) have cytostatic activity, and can be used in vaccine production and gene therapy. (I), (II), antibodies to (II), fusion proteins comprising (II), and isolated T cells prepared using (I) or (II) are used treat cancer in a patient. (I) and the antibodies are also used in the detection of cancer in a patient. (I) and (II) can be used in the detection of cancer in a patient. (I) and (II) can be used in vaccines. The antibodies or (I) can be used for monitoring the progression of cancer in a patient. (I) and (II) can be used to improve diagnostic and therapeutic methods for prostate cancer. They can indicate the level of metastasis as well as the prostate volume. AMPH9337 to AMPH93944 and AAM01115 to AAM01318 represent polymuclectide and anino acid sequences used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                        Harlocker SL, Jiang Y, Reed SG;
Retter MW, Stolk JA, Skeiky YAW
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                                                                                                                                                                                                                                                                                                                                                                                              New polynucleotide encoding a prostate-specific protein, monitoring and treating prostate cancer in a patient and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 325; 543pp; English
                                                                                                                                                                                                                        Dillon DC, Mitcham JL,
ID, Fanger GR, Day CH,
                                                     16-JAN-2001; 2001WO-US001574
                                                                                                             14-JAN-2000; 2000US-00483672
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Best Local Similarity 100.'
Matches 526; Conservative
                                                                                                                                                                                                                        Xu J, Dillon DC, Mi
Kalos MD, Fanger GR,
Wang A, Meagher MJ;
                                                                                                                                                                                                                                                                                                                                         WPI; 2001-425873/45
                                                                                                                                                                      (CORI-) CORIXA CORP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to isolated prostate-specific polynucleotides, polypeptides, fusion proteins of the polypeptides, antibodies raised against the polypeptides (or antigenic epitiopes derived from them) and antigen-presenting calls sorressing the polypeptides. The antibodies are useful for detecting the presence of cancer, especially prostate cancer. The polypeptides, polynucleotides and the antigen-presenting calls are useful for stimulating and/or expanding T calls specific for a tumour protein, and for inhibiting the development of cancer especially prostate cancer. Compositions comprising the polynucleotide and/or polypeptide are useful for stimulating an immune response, and for treating cancer. The oligonucleotide is useful for detecting cancer. The present sequence is a prostate specific polynucleotide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human prostate-specific polypeptides and polynucleotides useful for diagnosis and treatment of cancer, especially prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kalos MD;
Carter D;
                                                                                                                                                                                                Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.
                        526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; DB 4; Length 526;
4.5e-115;
            AGTICTATAAACTGTAGTNTACTTATTTTAATCCCCAAAGCACAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 526 BP; 177 A; 92 C; 86 G; 170 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 525;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 327; 579pp; English.
                                                                                                                                                                      Human prostate cDNA sequence #304
                                                                                        BP
                                                                                                                                                                                                                                                                                                                                                                                   2000US-00605783.
2000US-00636215.
2000US-00651236.
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                                                                                       AAS63752 standard; cDNA; 526
                                                                                                                                                                                                                                                                                                                                               2000US-00568100.
2000US-00570737.
2000US-00593793.
                                                                                                                                                                                                                                                                                                        27-MAR-2001; 2001WO-US009919
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                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                   WO200173032-A2.
                                                                                                                                                                                                                                                                                                                                                                                    27-JUN-2000;
09-AUG-2000;
29-AUG-2000;
06-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                         13-JUN-2000;
                                                                                                                                                                                                                                                                                                                                  27-MAR-2000;
                                                                                                                                                                                                                                                                                                                                               09-MAY-2000;
12-MAY-2000;
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                                                                                                                                           29-JAN-2002
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Li SX, Wa
481
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                                                               RESULT
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The present invention describes an isolated polypeptide (I) comprising at least an immunogenic portion of a prostate tumour antigen protein or its variant. (I) have cytostatic activity and can be used in vaccine production. (I), prostate tumour antigen polynucleotides, an antigen presenting cell (APC e.g. a dendritic cell) that expresses (I), and a pharmaceutical composition containing (I) are useful for inhibiting the
                                                                                                                                                                                                                                                                                    360
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61 TITIGACGITITICICIAAACTACTAAAGAGGGATTAATGATCCATAAAITATATTATTATCTA
                                                                        181 ATTAAACATGGAATAAAGATTTGTCCTTAAATATAAATCTACAAGAAGACTTTGATATTTG
                                                                                                                                                                                                                                                                                                                                                                                                     361 TCTCTTTACAGGGGGCTCCTGCAGCCCCTACAGAAATGAGTGGCTGAGATTCTTGATTGC
                                                  CATTTACAGGATTTAAAATGTGTTCAGCATGAAATATTAGCTACAGGGGAAGCTAAATAA
                                                                                                                               ATTAMACATGGAMTMAMGATTTGTCCTTMAMTMATAMTCTACAMGAMGACTTTGATATTTG
                                                                                                                                                                                                       TTTTTCACAAGTGAAGCATTCTTATAAAGTGTCATAACCTTTTTGGGGAAACTATGGGAA
                                                                                                                                                                                                                                              241 TTTTTCACAAGTGAAGCATTCTTATAAAGTGTCATAACCTTTTTGGGGAAACTATGGGAA
                                                                                                                                                                                                                                                                                                                        301 AAAATGGGGAAACTCTGAAGGGTTTTAAGTATCTTACCTGAAGCTACAGACTCCATAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                           ACAGCAAGAGCTTCTCATCTAAACCCTTTCCCTTTTTAGTATCTGTGTATCAAGTATAAA
                                                                                                                                                                                                                                                                                    AAAATGGGGAAACTCTGAAGGGTTTTAAGTATCTTACCTGAAGCTACAGACTCCATAAACC
                                                                                                                                                                                                                                                                                                                                                                 TCTCTTTACAGGGAGCTCCTGCAGCCCCTACAGAAATGAGTGGCTGAGATTCTTGATTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, prostate tumour antigen; prostate tumour; therapy, diagnosis;
prostate cancer; immunogenic; cytostatic; vaccine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGTICTATAAACTGTAGTNTACTTATTTTAATCCCCAAAGCACAGT 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGTICTATAAACTGTAGTNTACTTATTTTAATCCCCAAAGCACAGT 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Prostate tumour antigen determined cDNA sequence for P775P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAH02724 standard; cDNA; 526
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Best Local Similarity 100. Matches 526; Conservative

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development of cancer in a patient. Antibodies specific for prostate specific proteins and oligonucleotides that hybridise to a polynucleotide that encodes a prostate specific protein are useful for detecting the presence or absence of a cancer or monitoring the progression of a cancer, especially prostate cancer. AAH02422 to AAH2872, AAB7498 to AAB74821 and AAB74830 are sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                          240
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                                                                                                                                                                                                            CAAATTTGAGCCAATGACATAGAATTTTACAAATCAAGAAGCTTATTCTGGGGCCATTTC
                                                                                                                                                                                                                             CAAATTTGAGCCAATGACATAGAATTTTACAAATCAAGAAGCTTATTCTGGGGCCATTTC
                                                                                                                                                                                                                                                                                       TTTTGACGTTTTCTCTAAACTACTAAAGAGGCATTAATGATCCATAAATTATATTATCTA
                                                                                                                                                                                                                                                                                                                                 CATTTACAGCATTTAAAATGTGTTCAGCATGAAATATTAGCTACAGGGGAAGCTAAATAA
                                                                                                                                                                                                                                                                                                                                                   CATTTACAGCATTTAAAATGTGTTCAGCATGAAATATTAGCTACAGGGGAAGCTAAATAA
                                                                                                                                                                                                                                                                                                                                                                                          ATTAAACATGGAATAAAGATTTTGTCCTTAAATATATAATCTACAAGAAGACTTTGATATTTG
                                                                                                                                                                                                                                                                                                                                                                                                                       ATTAAACATGGAATAAAGATTTGTCCTTAAATATATAATCTACAAGAAGACTTTGATATTTG
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                                                                                                                                                Length 526;
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                                                                                                                     Sequence 526 BP; 177 A; 92 C; 86 G; 170 T; 0 U; 1 Other;
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Pred. No. 4.5e-115;
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0; Mismatches
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Matches 526; Conservative
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The present invention describes an isolated polypeptide (P1) comprising at least an immunogenic portion of a prostate-specific protein, or its variant. Also described are polymucleotides (N1) encoding (P1). (P1) and (N1) have cytostatic activity and can be used in vaccine production. The polypeptides, nucleic acids and antibodies from the present invention are useful in the diagnosis and therapy of prostate cancer. Prostate specific genes P704P, P712P, P774P, P775P and B305D are located in a genomic region on chromosome 22q11.2 known as the Cat Eye Syndrome region.

Prostate specific antigen (PSA) P501S was located on chromosome 1.

AAH84671 to AAH85143 and AAG99000 to AAG99077 represent polynucleotide and polypeptide sequences used in the exemplification of the present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                          Isolated polypeptide comprising at least an immunogenic portion of prostate-specific protein, useful in the diagnosis and therapy of
                                                                  Reed SG;
Wang A;
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                                                                    Harlocker SL, Jiang Y,
Day CH, Skeiky YAW,
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 526 BP; 177 A; 92 C; 86 G; 170 T; 0 U; 1 Other;
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100.0%; Pred. No. 4.5e-115;
ive 0; Mismatches 0;
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                                                                    Mitcham JL, I
99US-00439313
99US-00443686
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                                                                     Xu J, Dillon DC, Mit
Kalos MD, Retter MW,
                                                                                                                  WPI; 2001-308785/32.
                                         (CORI-) CORIXA CORP
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Matches 526; Conserv
                                                                                                                                                                          prostate cancer.
12-NOV-1999;
18-NOV-1999;
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us-09-232-880-311.rng

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Prostate specific protein and its encoding polynucleotide, useful for the treatment and diagnosis of prostate cancer.
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                361 TCTCTTTACAGGGAGCTCCTGCAGCCCCTACAGAAATGAGTGGCTGAGATTCTTGATTGC
                                                           ACAGCAAGAGCTTCTCATCTAAACCCTTTCCCTTTTTAGTATCTGTGTATCAAGTATAAA
TCTCTTTACAGGGAGCTCCTGCAGCCCCTACAGAAATGAGTGGCTGAGATTCTTGATTGC
                                                                                                                                                                                                                                                                                                                                                         Prostate cancer; vaccine; gene therapy; cytostatic; fusion protein; immunogen; cancer; prostate specific antigen; PSA; prostatic acid phosphatase; PAP; prostate specific membrane antigen; PSMA; gene; ss.
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Carter D;
Hural J;
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                                                                                                                       AGTICIATAAACTGTAGTNTACTTATTTTAATCCCCAAAGCACAGT
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                                                                                                                                                                                                                                                                                                                             Prostate cancer therapy associated cDNA #303.
                                                                                                                                                                                                                                 BP.
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04-OCT-2000; 2000US-00679272.
28-MAR-2001; 2001US-00822827.
                                                                                                                                                                                                                                 ACA59560 standard; cDNA; 526
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                                                                                                                                                                                                                                                                                               (first entry)
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HOUGHTON R L.
Y DE BASSOLS C V.
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WANG A.
SKEIKY Y A W.
HEPLER W T.
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KALOS M D.
FANGER G R.
RETTER M W.
STOLK J A.
DAY C H.
VEDVICK T S.
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MITCHAM J L.
HARLOCKER S I
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Mcneill PD,
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361
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(JIAN/)
(KALO/)
(FANG/)
(RETT/)
(STOL/)
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(WANG/)
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(MITC/)
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(HEND/)
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                                                                                                                                         gene;
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                                                                                                                                    Human; mouse; immunotherapy; cancer; leukaemia; WT1; Wilm's tumour chromosome 11p13; zinc finger transcription factor; ss.
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                                                                                                        Human P775P inventive antigen coding sequence SEQ ID NO: 336.
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                AAF86941 standard; cDNA;
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FANGER G R.
RETTER M W.
STOLK J A.
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VEDVICK T S.
CARTER D.
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MITCHAM J L.
HARLOCKER S I
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                 The invention describes a fusion protein comprising at least one amino acid sequence of immunogenic portions of any of the 3 sequences not defined in the specification, or sequences having at least 70 or 90 % sequence identity to any one of the 35 sequences defined in the USPTO web site, which is encoded by any of the 4 nucleotide sequences not defined in the specification. The fusion protein, composition and methods are useful for diagnosing, preventing and/or treating cancer, particularly prostate cancer. The proteins are useful as markers to indicate the presence or absence of cancer. This sequence represents a prostate cancer therapy associated cDNA. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the US patent office at sequence...
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Example 3; SEQ ID NO 311; 85pp; English
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The present invention provides prostate-specific coding sequences and their encoded proteins. These can be used in the diagnosis and treatment of cancers, particularly prostate cancer. The present sequence is a cDNA described in the invention
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and as markers for the
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100.0%; Score 525; DB 6; L
Best Local Similarity 100.0%; Pred. No. 4.5e-115;
Matches 526; Conservative 0; Mismatches 0;
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                                     97US-00806099.
97US-00904804.
98US-00030607.
98US-00115453.
98US-00115413.
99US-00159114.
99US-00159114.
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2000US-0058687.
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  CAAATTTGAGCCAATGACATAGAATTTTACAAATCAAGAAGCTTATTCTGGGGCCATTTC
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WD, Panger GR, Retter MW, Stolk JA, Day CH, Vedvick TS;
D, Li SX, Wang A, Skeiky YAW, Hepler WT, Hural J;
I PD, Houghton RL, Vinals Y De BassolsC, Foy TW, Watanabe
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29-JUN-2001; 2001US-00895814.
10-DEC-2001; 2001US-00012896.
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                                             The present invention relates to novel prostate-specific proteins (PSP) and their coding sequences. The PSPs and their coding sequences are useful for stimulating an immune response in a patient, or for treating prostate cancer in a patient and for determining, detecting or diagnosing the presence of a cancer in a patient. The present sequence was used to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTTTGACGTTTTCTCTAAACTACTAAAGAGGCATTAATGATCCATAAATTATATTATCTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                     CAAATTTGAGCCAATGACATAGAATTTTACAAATCAAGAAGCTTATTCTGGGGCCATTTC
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                                                                                                                                                                                                                            Sequence 526 BP; 177 A; 92 C; 86 G; 170 T; 0 U; 1 Other;
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                                                                                                                                                                                                                                                                               Score 525; DB 8; I
Pred. No. 4.5e-115;
O; Mismatches O;
Example 3; Page 392-393; 691pp; English.
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100.0%;
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                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 526; Conservative
                                                                                                                                                                              illustrate the invention
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The invention relates to an isolated polypeptide comprising no more than 11-542 amino acids of ADB13563 comprising a sequence ADB14487. The peptides comprises a fragment ADB13563 of that contain naturally processed T-cell epitopes for 3 class I major histocompatibility complex (MHC) alleles. ADB13563 is a polypeptide encoded by a human prostate specific companion one of 648 disclosed as new. Also included are nucleic acids encoding the proteins and peptide, expression vectors, a host cell transformed with the vector, an isolated antibody (or antigen binding crassifically binds to the protein or peptide, detecting the presence of a cancer in a patient (comprising contacting a patient cample with a binding agent that binds to the peptide or a polypeptide to appearing as ADB13563, detecting the amount of polypeptide to a prodetermine to the presence of cancer), a fusion protein of value to determine the presence of cancer), a fusion protein comprising the peptides or proteins, stimulating or expanding T cells specific for a tumour protein comprising contacting T cells with the peptides or troteins, stimulating or expanding T cells peptides or the isolated T cell population, treating prostate cancer in a patient and treating prostate cancer in a patient and treating prostate cancer in a patient and treating prostate cancer in a patient with the peptides or compounds, determining the presence of cancer in a patient with the peptides or antigen presenting cells that express (the peptides to the patient. The peptides (or an oligonuclectide concer the thybridises to nucleic acid encoding them), is used to detect the presence of cancer in a patient. The peptides, nucleic acid sencoding, or antigen-presenting cells expressing the nucleic acid, are used to antigen-presenting cells expressing the nucleic acid, senceding, the protein and patient. The peptides or concerns a patient with the peptides or antigen presence of cancer in a patient. The peptides or antigen presence of cancer in a patient or the patient. The peptide
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                                                                                                                            98US-00030607.
98US-00115453.
98US-00115453.
99US-00232149.
99US-00288946.
99US-00352616.
99US-0043368.
2000US-00443686.
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2000US-00709729.
2001US-00759143.
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2000US-00657279.
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2000US-00605783.
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2001US-00895814
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                                    2002US-00294025
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13-JUL-1999;
12-NOV-1999;
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13-JUN-2000;
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09-AUG-2000;
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                                    12-NOV-2002;
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                   or antigen
                                                                                                                                                                                                                                                       9
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stimulate or expand T cells specific for a tumour protein. The peptides, nucleic acids, antibodies, fusion proteins, T cell populations or antige presenting cells are used to stimulate an immune response or treat prostate cancer in a patient. The present sequence is one of the disclosed human prostate specific CDNAs. Note: Except where otherwise indicated, the sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                              1 CAAATTTGAGCCAATGACATAGAATTTTACAAATCAAGAAGCTTATTCTGGGGCCATTTC
                                                                                                                                                                                                                                                                                      TTTTGACGTTTTCTCTAAACTACTAAAGAGGCATTAATGATCCATAAATTATATTATCTA
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                                                                                                                                                                                                Gaps
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                                                                                                        from USPTO at segdata.uspto.gov/sequence.html?DocID=20030185830
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0
                                                                                                                                                                 Length 526;
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                                                                                                                                     Sequence 526 BP; 177 A; 92 C; 86 G; 170 T; 0 U; 1 Other;
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                                                                                                                                                                 100.0%; Score 525; DB 10; 100.0%; Pred. No. 4.5e-115;
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                                                                                                                                                                                              0; Mismatches
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                                                                                                                                                                                                526; Conservative
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ACAGCAAGAGCTTCTCATCTAAACCCTTTCCCTTTTTAGTATCTGTGTATCAAGTATAAA 480
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                       CATTTACAGCATTTAAAAATGTGTTCAGCATGAAATATTAGCTACAGGGGAAGCTAAAATAA
                                                                                       AAAATGGGGAAACTCTGAAGGGTTTTAAGTATCTTACCTGAAGCTACAGACTCCATAACC
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      CATTTACAGCATTTAAAATGTGTTCAGCATGAAATATTAGCTACAGGGGAAGCTAAATAA
                                                                      ATTAAACATGGAATAAAGATTTGTCCTTAAATATAAATCTACAAGAAGACTTTGATATTTG
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Day CH, Vedvick TS;
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97US-00204804.
98US-00020607.
98US-00115453.
98US-00159812.
99US-00232149.
99US-00352616.
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99US-00443686.
2000US-00483672.
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2000US-00568100
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27-MAR-2000;
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09-APR-1999;
13-JUL-1999;
12-NOV-1999;
18-NOV-1999;
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01-AUG-1997;
09-FEB-1998;
25-FEB-1998;
14-JUL-1998;
23-SEP-1998;
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Kalos MD,
Carter D,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to human prostate-specific polypeptides and the polymucleotides encoding them. The invention also relates to an isolated antibody or its antigen-binding fragment that specifically binds a polypeptide of the invention, a method of detecting cancer in a parient comprising contacting a biological sample of the patient with an agent that binds a prostate-specific polypeptide and comparing the amount of bound polypeptide comparated to a predeternmined cut-off value and a fusion protein comprising a prostate-specific polypeptide. The sequences of the invention are used to diagnose and treat cancer, particularly prostate cancer. This sequence represents cDNA encoding a human prostate-specific polypeptide of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polynucleotides encoding prostate specific polypeptides isolated from a human prostate tumor cDNA library are useful to diagnose and treat
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Kalos MD, Fanger GR, Retter MW, Stolk JA, Day CH, Vedv
Carter D, Li SX, Wang A, Skeiky YAW, Hepler WT, Hural
Mcneill PD, Houghton RL, Vinals Y De BassolsC, Foy TM, theagher MJ, Deng T;
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97US-00806099.
97US-00904804.
98US-00030607.
98US-00115453.
98US-00115453.
99US-001581149.
99US-00288946.
99US-0048946.
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2000US-00536857.
2000US-00576110.
2000US-00593793.
2000US-00693783.
2000US-00605783.
2000US-00657236.
2000US-00657279.
2000US-00657279.
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2001US-00759143.
2001US-00780669.
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Matches 526; Conservative
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27-MAR-2000;
09-MAY-2000;
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06-SEP-2000;
02-OCT-2000;
10-OCT-2000;
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09-FEB-2001;
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29-JUN-2001;
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15-JAN-1999;
09-APR-1999;
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13-JUN-2000;
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                                                    25-FEB-1998
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18-JUL-2000;
13-DEC-2000;
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16-MAR-2000;
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          23-AUG-2001
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                                                 The present invention relates to prostate-specific fusion proteins and DNA encoding sequences. The fusion proteins can be used for diagnosing, preventing, or treating cancer, such as prostate cancer. The prostate specific proteins were isolated from a human prostate tumor cDNA library. The present sequence is one such cDNA clone which was isolated in the prostate-specific CDNA library. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html.
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 or treating cancer,
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100.0%; Pred. No. 4.5e-115;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human prostate expression marker cDNA 27587
useful for diagnosing, preventing,
                               Example 3; SEQ ID NO 311; 78pp; English
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            cancer
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The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV0010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether progression of prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) assessing the prostate cancer in a patient; (f) assessing the prostate call carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (l) assessing the aggressiveness or indolence of prostate cancer in a patient; (I) is also useful as a pharmacodyanamic or pharmacogenomic marker
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                                                                                                                                                                                                                                                                                                                                                                                                                  Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1203 BP; 395 A; 209 C; 199 G; 391 T; 0 U; 9 Other;
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                                                                                                                                                                                                                                                     INC.
                                                                                                                                                                                                                                                        (MILL-) MILLENNIUM PREDICTIVE MEDICINE
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                                                                                                                                                                                                                                                                                                             Monahan JE;
                                                  2000US-0183319P.
2000US-0189662P.
2000US-0207454P.
2000US-0211314P.
2000US-021907P.
20-FEB-2001; 2001WO-US005171
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Matches 512; Conservative
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521

360

701

641

420

761

480

819

g 8 g

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The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether
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                     CATTTACAGCATTTAAAATGTGTTCAGCATGAAATATTAGCTACAGGGGAAGCTAAATAA
                                            522 ATTAAACAIGGAATAAAGATTIGICCTIAAATATAATCTACAAGAAGACTITGATATTIG
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pharmacogenomic marker;
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25-MAY-2000;
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                                        AGTICTATAAACTGTAGTNTACTTATTTTAATCCCCAA
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a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate call carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (l) is also useful as a pharmacodyanamic or pharmacogenomic marker
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BD242216 52003 S26 bp DNA linear PAT 17-JUL-2003 Compounds for immunotherapy and diagnosis of prostate cancer and methods for their use.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Dillon,D.C., Harlocker,S.L., Yuqiu,J., Xu,J. and Mitcham,J.L.
Compounds for immunotherapy and diagnosis of prostate cancer and methods for their use
Patent: JP 2002520054-A 303 09-JUL-2002;
CORIXA CORP
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Location/Qualifiers
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/organism="Homo sapiens"
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CQ495503
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CQ511185
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AP000528
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AR400377
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BD242216.1 GI:33051986
JP 2002520054-A/303.
Homo sapiens (human)
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AR278423 Sequence
AR371015 Sequence
AR371015 Sequence
AR401015 Sequence
AR40522 Sequence
AR439626 Sequence
AR53802 Sequence
AR53802 Sequence
AR566947 Sequence
AR666947 Sequence
AR716854 Sequence
AX106530 Sequence
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AX10630 Sequence
AX10631 Sequence
AX10631 Sequence
AX26631 Sequence
AX266331 Sequence
                                                                                                    December 31, 2006, 12:13:09; Search time 3386.49 Seconds (without alignments) 9932.518 Million cell updates/sec
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               GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd
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Maximum Match 100%
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AR371015
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llarity 100.0%; Pred. No. 2.3e-138;
Conservative 0; Mismatches 0;
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Corixa Corporation; Seattle, WA
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    /organism="unknown"
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                                                             Length 526;
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; Pred. No. 2.3e-138;
0; Mismatches 0;
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Xu,J., Dillon,D.C. and Mitcham,J.L.
Compounds for immunotherapy of prostate
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Patent: US 6465611-A 311 15-OCT-2002;
Corixa Corporation; Seattle, WA
Location/Qualifiers
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AR237399
AR237399.1 GI:27282057
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larity 100.0%;
Conservative 0;
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DEFINITION ACCESSION VERSION KEYWORDS SOURCE

RESULT 2 AR237399 LOCUS

ORGANISM REFERENCE AUTHORS source

ORIGIN

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FEATURES

JOURNAL

TITLE

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Matches 526; Conservative 0; Mismatches 0;
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Corixa Corporation; Seattle, WA;
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/organism="unknown"
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Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H., Vedvick,T.S., Carter,D., S.X., Wang,A., Skeiky,Y.A.W., Hepler,W.T. and Henderson,R.A.

Compositions and methods for the therapy and diagnosis of pr
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llarity 100.0%; Pred. No. 2.3e-138;
Conservative 0; Mismatches 0;
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Corixa Corporation; Seattle, WA
Location/Qualifiers
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    organism="unknown"
    /mol_type="genomic DNA"

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Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,

Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,

Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,

Hepler,W.T. and Henderson,R.A.

Compositions and methods for the therapy and diagnosis of prostate
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      Hepler, W.T. and Henderson, R.A. Compositions and methods for the therapy and diagnosis of cancer
//edvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,
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Best Local Similarity 100.0%; Pred. No. 2.3e-138;
Matches 526; Conservative 0; Mismatches 0;
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Corixa Corporation; Seattle, WA
Location/Qualifiers
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Patent: US 6800746-A 311 05-OCT-2004;
Corixa Corporation; Seattle, WA
Location/Qualifiers
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/wol_type="genomic DNA"
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Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
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Matches 526; Conservative 0; Mismatches 0;
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Corixa Corporation; Seattle, WA;
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Sequence 311 from patent US 6759515.
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AR563802.1 GI:53978853
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1. .526
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DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

RESULT 9 AR563802

REFERENCE AUTHORS

	Oy 61 TTTTGACGTTTTCTCTAAACTACGAGGGCATTAATGATCCATAATTATTATCTA 120	181 ATTAAACATGGAATAAAGATTTGTCCTTAAATATAATCTACAAGAAGACTTTGATATTTG	Oy 241 TTTTCACAAGTGAAGCATTCTTATAAAGTGTCATAACCTTTTTGGGGAAACTATGGGGA 300	301 AAAATGGGGAAACTCTGAAGGGTTTTAAGTATCTTACCTGAAGCTACACATAACC 361 TCTCTTTACAGGGAGCTCCTGCAGCCCCTACAGAAATGAGTGGCTGAAATTGCTTACTTA	361 421	?	SULT 12	AR656947 526 bp DNA linear PAT 13-JUN-2005 LOCUS DEFINITION Sequence 311 from patent US 6894146. ACCESSION AR656947 GI:67590059		Cancer: US 6894146-A 311 17-MAY-2005; Corixa Corporation; Seattle, WA FEATURES Location/Qualifiers Source 1526 /organism="unknown" /mol_type="genomic DNA"	Query Match 100.0%; Score 525; DB 2; Length 526; Best Local Similarity 100.0%; Pred. No. 2.3e-138; Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Oy 1 CAAATTTGAGCCAATGACATAGAATTTTACAAAAGCTTATTCTGGGGCCATTTC 60	Qy 61 TTTTGACGTTTTCTCTAAACTACTAAAGAGGCATTAATGATCCATAAATTATATTATCTA 120
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
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CORIXA CORPORATION (US)
LOCATION/Qualifiers
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1. .526
/note="n = A,T,C or G"
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Sequence 311 from Patent W00125272.
AX106530 AX106530.1 GI:13922208
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Sequence 380, App Sequence 3267, Ap

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Sequence 12707, A Sequence 294, App Sequence 568, App Sequence 1267, App Sequence 6524, App Sequence 201282, Sequence 201283, Sequence 1313, App Sequence 1313, App Sequence 1313, App Sequence 1313, App Sequence 1313, App

Sequence 6304, Ap Sequence 5907, Ap

ALIGNMENTS

Sequence 1211,

Sequence 332, App Sequence 218, App

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APPLICANT: Watanabe, Yoshihiro
APPLICANT: Meagher, Madeleine Joy
APPLICANT: Deng, Ta
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSITATE CANCER
FILE REFERENCE: 210121.427C32
                                     0 US-11-299-286-3267

0 US-11-299-286-3267

US-11-204-780-4586

US-11-266-748A-400197

US-11-266-748A-471243

US-11-266-748A-471243

US-11-348-441-294

US-10-517-441-588

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US-11-266-748A-201283

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US-11-266-989-314

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CURRENT FILING DATE: 2006-02-01
PRIOR APPLICATION NUMBER: US/144,678
PRIOR APPLICATION NUMBER: 10/144,678
PRIOR FILING DATE: 2002-05-09
PRIOR PILING DATE: 2001-12-10
PRIOR FILING DATE: 2001-12-10
PRIOR PLING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-29
PRIOR PLING DATE: 2010-06-99
PRIOR PLING DATE: 2010-06-99
PRIOR PLING DATE: 2010-06-99
PRIOR FILING DATE: 2010-06-09
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Publication No. US20060269532A1
GENERAL INFORMATION:
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
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Houghton, Raymond L.
Vinals y de Bassols, C
Foy, Teresa M.
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Skeiky, Yasir A. W.
Hepler, William T.
Hural, John
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Vedvick, Thomas S.
Carter, Darrick
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Retter, Marc W.
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| FEMC_Celerra_SIDS3/ptodata/2/pubpna/USO3_NEW_PUB.seq:*
| FEMC_Celerra_SIDS3/ptodata/2/pubpna/USO3_NEW_PUB.seq:*
| FEMC_Celerra_SIDS3/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
| FEMC_Celerra_SIDS3/ptodata/2/pubpna/USI3_NEW_PUB.seq:*
| FEMC_Celerra_SIDS3/ptodata/2/pubpna/USI1_NEW_PUB.seq:*
| FEMC_Celerra_SIDS3/ptodata/2/pubpna/USI1_NEW_PUB.seq:*
| FEMC_Celerra_SIDS3/ptodata/2/pubpna/USI1_NEW_PUB.seq2:*
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| FEMC_Celerra_SIDS3/ptodata/2/pubpna/USI1_NEW_PUB.seq2:*
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                      GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd
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PRIOR APPLICATION NUMBER: 09/759,143
PRIOR FILING DATE: 2001-01.12
PRIOR PILING DATE: 2001-01.12
PRIOR FILING DATE: 2000-11-09
PRIOR FILING DATE: 2000-10.10
PRIOR PILING DATE: 2000-10.10
PRIOR PILING DATE: 2000-10.02
PRIOR APPLICATION NUMBER: 09/679,426
PRIOR PILING DATE: 2000-00.2
PRIOR APPLICATION NUMBER: 09/657,279
PRIOR FILING DATE: 2000-09-06
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NUMBER OF SEQ ID NOS: 1033
SOFTWARE: PASESEQ for Windows Version 3.0
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Best Local Similarity 100.
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US-11-344-932-476/C

Sequence 476, Application US/11344932

Publication No. US20060269532A1

GENERAL INPORMATION:

APPLICANT: Xu, Jiangchun

APPLICANT: Mitcham, Jennifer L.

APPLICANT: Mitcham, Jennifer L.

APPLICANT: Harlocker, Susan L.

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3002 TTTTGACGTTTTCTCTAAACTACTAAAGAGGCATTAATGATACATAAATACATTATCTA 2943
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APPLICANT: Deng, Ta
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
TITLE REFERENCE: 210121,427622
CURRENT APPLICATION NUMBER: US/11/344,932
CURRENT FILING DATE: 2006-02-01
PRIOR FILING DATE: 2006-02-09
PRIOR PLING DATE: 2001-12-10
PRIOR PLING DATE: 2001-12-10
PRIOR PLING DATE: 2001-06-29
PRIOR PLING DATE: 2001-06-29
PRIOR PLING DATE: 2001-06-29
PRIOR PLING DATE: 2001-06-99
PRIOR PLING DATE: 2001-05-09
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                                                                                                                                                                                                                                                                                                                                     MCNeill, Patricia D.
Houghton, Raymond L.
Vinals y de Bassols, Carlota
Foy, Teresa M.
Matanabe, Yoshihiro
Maagher, Madeleine Joy
Deng, Ta
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Vedvick, Thomas S.
Carter, Darrick
Li, Samuel X.
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Hepler, William T.
Jiang, Yuqiu
Henderson, Robert
Kalos, Michael D.
                                                                       Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
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ORGANISM: Homo sapiens
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61 TITIGACGITITICICIAAACTACTAAAGAGGCATTAATGATCCATAAATTATATTATCTA 120
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PRIOR FILING DATE: 2000-10-10
PRIOR APPLICATION NUMBER: 09/679,426
PRIOR FILING DATE: 2000-10-02
PRIOR PLING DATE: 2000-06
PRIOR PLING DATE: 2000-09-06
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1033
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 475
LENGTH: 2414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                           49.8%; Score 261.6; DB 7; Length 2414; 98.1%; Pred. No. 7.3e-56; tive 0; Mismatches 5; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 TITITCACAAGIGAAGCATICITATAAAG 269
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Publication No. US20060269532A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: n = A,T,C or G
US-11-344-932-475
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Meagher, Madeleine Joy
Deng, Ta
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Jiang, Yuqiu
Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
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Hepler, William T.
Hural, John
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Vedvick, Thomas S.
Carter, Darrick
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Best Local Similarity 98.1;
Matches 264; Conservative
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                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
LOCATION: 33
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                                                                                               2822 TTTTTCACAAGTGAAGCATTCTTATAAAGTGTCATAACCTTTTTGGGGAAACTATGGGAA 2763
    2882 ATTAAACATGGAATAAAGATTTGTCCTTAAAAATAATCTACAAGAAGACTTTGATATTTG 2823
                                                                                                                                                                                                                                      420
                                                   241 TITITCACAAGIGAAGCAIICITATAAAGIGICATAACCIITITIGGGGAAACTAIGGGAA 300
                                                                                                                                                                                                                                                                                                                                   421 ACAGCAAGAGCTTCTCATCTAAACCCTTTTCCCTTTTTAGTATCTGTGTATCAAGTATAAA 480
                                                                                                                                                                                                                                                                                    2702 TCTCTTTACAGGGAGCTCCTGCAGCCCCTACAGAAATGAGTGGCTGAGATTCTTGATTGC
                                                                                                                                         301 AAAATGGGGAAACTCTGAAGGGTTTTAAGTATCTTACCTGAAGCTACAGACTCCATAACC
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Houghton, Raymond L.
Vinals y de Bassols, Carlota
Foy, Teresa M.
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RRIOR FILING DATE: 2002-05-09
RRIOR FILING DATE: 2002-05-09
RRIOR FILING DATE: 2001-12-10
PRIOR PELICATION NUMBER: 10/012,896
PRIOR APPLICATION NUMBER: 09/895,814
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-09
PRIOR PELING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 09/780,669
PRIOR APPLICATION NUMBER: 09/789,143
PRIOR APPLICATION NUMBER: 09/799,143
PRIOR PELING DATE: 2001-01-12
PRIOR FILING DATE: 2001-01-12
PRIOR FILING DATE: 2001-01-12
PRIOR FILING DATE: 2001-01-12
PRIOR PELING DATE: 2001-01-10-09
PRIOR FILING DATE: 2001-01-10-09
PRIOR FILING DATE: 2001-01-09
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8-11-344-932-475/c
; Sequence 475, Application US/11344932
; Publication No. US20060269532A1
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Meagher, Madeleine Joy
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APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
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Skeiky, Yasir A. W.
Hepler, William T.
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Vedvick, Thomas S
Carter, Darrick
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Retter, Marc W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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AFPLICANT: HOEFLER, Heinz

TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cell
TITLE OF INVENTION: Proliferative disorders
TITLE OF INVENTION: Proliferative disorders
FILE REFERENCE: 47675-93
CURRENT APPLICATION NUMBER: US/10/517,441
CURRENT APPLICATION NUMBER: D04-12-11
FRIOR APPLICATION NUMBER: PCT/EP2003/010881
FRIOR APPLICATION NUMBER: DE 10317955.0
FRIOR FILING DATE: 2003-04-17
FRIOR APPLICATION NUMBER: DE 10300096.8
FRIOR APPLICATION NUMBER: DE 10245779.4
FRIOR FILING DATE: 2002-10-01
FRIOR FILING DATE: 2002-10-01
FRIOR FILING DATE: 2002-10-01
FRIOR FILING DATE: 2002-10-01
FRIOR APPLICATION NUMBER: DE 10245779.4
FRIOR FILING DATE: 2002-10-01
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FRIOR FILING DATE: 2002-10-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 8.7%; Score 45.8; DB 6; Length 4022; Best Local Similarity 51.2%; Pred. No. 0.11; Matches 107; Conservative 0; Mismatches 102; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1981 AAATCAAATTTTAATTAAATTATCATAA 1953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 249 AAGTGAAGCATTCTTATAAAGTGTCATAA 277
      PRIOR FILING DATE: 2003-04-17
PRIOR APPLICATION NUMBER: DE 10300096.8
PRIOR FILING DATE: 2003-01-07
PRIOR PELLING DATE: 2002-10-01
PRIOR FILING DATE: 2002-10-01
NUMBER OF SEQ ID NOS: 2147
SEQ ID NO 458
LENGTH: 4022
                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION: (1299, 1372, 1784, 3008, 3018)
; OTHER INFORMATION: unknown base
US-10-517-441-458
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Publication No. US20060121467A1
GENERAL INFORMATION:
APPLICANT: FOEKENS, John
APPLICANT: HARBECK, Nadia
APPLICANT: KOENIG, Thomas
                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SCHMITT, Armin
SCHMITT, Manfred
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MODEL, Fabian
NIMMRICH, Inko
RUJAN, Tamas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KOENIG, Thomas
MAIER, Sabine
                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: unsure
LOCATION: (1299,
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APPLICANT:
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TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cel
TITLE OF INVENTION: proliferative disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           109 CAAATTTGAGCCAATGACATAGAATTTTACAAATCAAGAAGCTTATTCTGGGGCCATTTC 50
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER CURRENT 21012.42763

FILE REFERENCE: 21012.42763

CURRENT PAPLICATION UNMERS: US/11/344,932

CURRENT FILING DATE: 2006-02-01

PRIOR APPLICATION NUMBER: 10/144,678

PRIOR FILING DATE: 2001-05-09

PRIOR FILING DATE: 2001-05-09

PRIOR FILING DATE: 2001-06-29

PRIOR FILING DATE: 2001-06-29

PRIOR FILING DATE: 2001-06-09

PRIOR FILING DATE: 2001-06-09

PRIOR FILING DATE: 2001-05-09

PRIOR FILING DATE: 2001-05-09

PRIOR FILING DATE: 2001-01-12

PRIOR PAPLICATION NUMBER: 09/789,143

PRIOR PAPLICATION NUMBER: 09/789,143

PRIOR PAPLICATION NUMBER: 09/789,143

PRIOR PAPLICATION NUMBER: 09/709,729

PRIOR PAPLICATION NUMBER: 09/709,729

PRIOR PAPLICATION NUMBER: 09/65,166

PRIOR PAPLICATION NUMBER: 09/65,166

PRIOR PAPLICATION NUMBER: 09/65,279

PRIOR PLING DATE: 2000-110-09

PRIOR PILING DATE: 2000-10-10

PRIOR PILING DATE: 2000-10-10

PRIOR PILING DATE: 2000-10-01

PRIOR PILING DATE: 2000-10-01

PRIOR PILING DATE: 2000-10-01

PRIOR PILING DATE: 2000-10-01

PRIOR PILING DATE: 2000-10-01

PRIOR PILING DATE: 2000-10-01

PRIOR PILING DATE: 2000-10-01
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 474
LENGTH: 1594
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CURRENT FILING DATE: 2004-12-11
PRIOR APPLICATION NUMBER: PCT/EP2003/010881
PRIOR FILING DATE: 2003-10-01
PRIOR APPLICATION NUMBER: DE 10317955.0
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Publication No. US20060121467A1
GENERAL INFORMATION:
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SCHMITT, Armin
SCHMITT, Manfred
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KOENIG, Thomas
MAIER, Sabine
MARTENS, John
MODEL, Fabian
NIMMRICH, Inko
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MARX, Almuth
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US-11-344-932-474
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APPLICANT:
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us-09-232-880-311.rnpbn

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US-11-299-286-2856/c

Sequence 2856, Application US/11299286

Publication No. USCO60183137A1

GENERAL INFORMATION:

APPLICANT: Kreps, Joel

APPLICANT: Kreps, Joel

APPLICANT: Wang, Yun

APPLICANT: Any Tong

TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING

TITLE OF INVENTION: SAME, AND METHODS OF USE

FILLE REFERENCE: SCRIP1300-3

CURRENT APPLICATION NUMBER: US/11/299,286

CURRENT FILLING DATE: 2005-12-09
                                                                                                                                                                                                              9739 AITTITATTTTTTGAATTATAATATATTAAGAAATGTAAATTGTGATTAGATTTATTT 9798
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                                                                                                        9799 ATATITITTAGAATATIATGAAATGIGITITIAAATATGITTAATTGATTTAGAATTTTAGAAATTTT 9858
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                                                    94 TTAATGATCCATAAATTATTATCTACATTTACAGCATTTAAAAATGTTTCAGCATGAA
                                                                                                                                                            154 ATATTAGCTACAGGGAAGCTAAATAAATTAAACATGGAATAAAGATTTGTCCTTAAATA
                                                                                                                                                                                                                                                                     214 TAATCTACAAGAAGACTTTGATATTTGTTTTTCACAAGTGAAGCATTCTTATAAAGTGTC
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     Gaps
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  87; Indels
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8.1%; Score 42.4; DB 10;
Best Local Similarity 49.1%; Pred. No. 0.62;
Matches 112; Conservative 0; Mismatches 116;
     Mismatches
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PRIOR FILING DATE: 2001-08-24
PRIOR PFLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2001-01-16
PRIOR PLILING DATE: 2001-01-16
PRIOR PLILING DATE: 2001-01-05
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEO ID NOS: 5379
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     95; Conservative
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TITLE OF INVENTION: proliferative disorders
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                                                                               OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
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Pred. No. 0.91;
                                                                                                                                                                                                                                                                        Length 4022;
                                                                                                                                                                                                                                                                  Score 45.8; DB 6; Length 4
Pred. No. 0.11;
0; Mismatches 102; Indels
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CURRENT FILING DATE: 2004-12-1.
FURKENT FILING DATE: 2004-12-1.
PRIOR APPLICATION NUMBER: PCT/EP2003/010881.
PRIOR FILING DATE: 2003-10-0.
PRIOR FILING DATE: 2003-0.1.
PRIOR APPLICATION NUMBER: DE 10317955.0.
PRIOR APPLICATION NUMBER: DE 10300096.8.
PRIOR FILING DATE: 2003-01-07.
PRIOR FILING DATE: 2003-01-07.
PRIOR FILING DATE: 2003-10-01.
PRIOR FILING DATE: 2003-10-01.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               249 AAGTGAAGCATTCTTATAAAGTGTCATAA 277
                                                                                                                                    ; NAME/KEY: unsure
; LOCATION: (1299, 1372, 1784, 3008, 3018)
; OTHER INFORMATION: unknown base
US-10-517-441-732
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Publication No. US20060121467A1
                           ORGANISM: Artificial Sequence
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APPLICANT: HARBECK, Nadia
APPLICANT: KOENIG, Thomas
APPLICANT: MAIER, Sabine
APPLICANT: MARTENS, John
APPLICANT: MODEL, Fabian
APPLICANT: NIMMRICH, INKO
APPLICANT: RUJAN, Tamas
APPLICANT: SCHMITT, Armin
APPLICANT: SCHMITT, Armin
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 51.2%;
Matches 107; Conservative
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MARX, Almuth
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 47675-93
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Best Local Similarity
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LENGTH: 13286
                                                                                                           FEATURE:
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APPLICANT: Schmitt, Armin
TITLE OF INVENTION: METHOD AND NUCLEIC ACIDS FOR THE ANALYSIS OF A COLON CELL PROLIFE.
TITLE OF INVENTION: DISORDER
FILTE OF INVENTION: DISORDER
FILTE OF INVENTION: DISORDER
FILTE OF INVENTION: DISORDER
FILTE OF INVENTION: DISORDER
FILTE OF INVENTION: DISORDER: US/10/506,111
CURRENT APPLICATION NUMBER: US/10/506,111
PRIOR APPLICATION NUMBER: PT/EP03/02035
PRIOR FILING DATE: 2003-02-27
PRIOR FILING DATE: 2003-02-27
NUMBER OF SEQ ID NOS: 1030
SEQ ID NO 346
LENGTH: 6432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cel
TITLE OF INVENTION: proliferative disorders
FILE REFERENCE: 47675-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97 ATGATCCATAAATTATATTATCTACATTTACAGCATTTAAAAATGTGTTCAGCATGAAATA 156
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                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-506-111-346
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 6432;
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Pred. No. 0.9;
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; Publication No. US20060121467A1
; GENERAL INFORMATION:
A APPLICANT: FOBEENS, John
; APPLICANT: HARBECK, Nadia
APPLICANT: MAIER, Sabine
A APPLICANT: MAIER, Sabine
A APPLICANT: MARTENS, John
; APPLICANT: MODEL, Fabian
; APPLICANT: NIMMRICH, Inko
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                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Artificial Sequence
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SCHMITT, Armin
SCHMITT, Manfred
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MARX, Almuth
HOEFLER, Heinz
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Best Local Similarity 47.6
Matches 159; Conservative
Becker, Evelyne
Lesche, Ralf
                                          Rujan, Tamas
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APPLICANT:
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TITLE OF INVENTION: proliferative disorders
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8.1%; Score 42.4; DB 6; Length 6432;
Best Local Similarity 47.6%; Pred. No. 0.9;
Matches 159; Conservative 0; Mismatches 171; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3287 ATTCAATCCACAAAACCAAAAATTAACTAAATA 3254
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PRIOR PELICATION NUMBER: PCT/EP2003/010881
PRIOR FILING DATE: 2003-10-01
PRIOR FILING DATE: 2003-04-17
PRIOR FILING DATE: 2003-04-17
PRIOR FILING DATE: 2003-01-07
PRIOR PILING DATE: 2003-01-07
PRIOR APPLICATION NUMBER: DE 10245779-4
PRIOR FILING DATE: 2002-10-01
PRIOR FILING DATE: 2002-10-01
PRIOR FILING DATE: 2002-10-01
SEQ ID NO 606
LENGTH: 6432
                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 47675-93
CURRENT APPLICATION NUMBER: US/10/517,441
CURRENT FILING DATE: 2004-12-11
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Publication No. US20060246433A1
GENERAL INFORMATION: APPLICANT: Adorjan, Peter
APPLICANT: Burger, Matchias
APPLICANT: Maier, Sabine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                       SCHMITT, Armin
SCHMITT, Manfred
                                                                                                                                                                                                               LOOK, Maxime P.
MARX, Almuth
HOEFLER, Heinz
    FOEKENS, John
HARBECK, Nadia
KOENIG, Thomas
MAIER, Sabine
                                                                                                                              NIMMRICH, Inko
RUJAN, Tamas
                                                                                     MARTENS, John
MODEL, Fabian
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APPLICANT:
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APPLICANT: Modian, Peter
APPLICANT: Burger, Matthias
APPLICANT: Burger, Matthias
APPLICANT: Burger, Matthias
APPLICANT: Lesche, Ralf
APPLICANT: Cottrell, Susan
APPLICANT: Mooney, Suzanne
TITLE OF INVENTION: Method and nucleic acids for the analysis of colon cell prolifers
TITLE OF INVENTION: 4180rders
TITLE OF INVENTION: 4180rders
CURRENT APPLICATION NUMBER: US/10/506,089
CURRENT FILING DATE: 2004-08-27
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                                                                                                                ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-517-441-564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
                                                                                                                                                                                     DB 6; Length 16579;
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Pred. No. 1.4;
0; Mismatches 113; Indels
                                                                                                                                                                                                                                 0; Mismatches 113; Indels
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Pred. No. 1.
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PRIOR FILING DATE: 2003-02-27
PRIOR APPLICATION NUMBER: EP 02004551.4
PRIOR FILING DATE: 2002-02-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 9, Application US/10506089; Publication No. US20060234224A1
                                              TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                Query Match 8.0%;
Best Local Similarity 49.3%;
Matches 110; Conservative
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Best Local Similarity 49.3%;
Matches 110; Conservative
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US-10-506-089-9
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                                                                                             FEATURE:
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APPLICANT: HOEFLER, Heinz
TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cel
TITLE OF INVENTION: proliferative disorders
FILE REFERENCE: 47675-93
CURRENT APPLICATION NUMBER: US/10/517,441
CURRENT FILING DATE: 2004-12-11
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Pred. No. 1.4;
0; Mismatches 113; Indels 0;
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PRIOR PLING DATE: 2004-12-11

PRIOR FILING DATE: 2003-10-01

PRIOR FILING DATE: 2003-10-01

PRIOR FILING DATE: 2003-04-17

PRIOR FILING DATE: 2003-04-17

PRIOR PLICATION NUMBER: DE 1031095.8

PRIOR FILING DATE: 2003-01-07

PRIOR FILING DATE: 2003-01-07

PRIOR FILING DATE: 2002-10-01

NUMBER OF SEQ ID NOS: 2147
                                                      CURRENT FILING DATE: 2004-12-11
FRIOR APPLICATION NUMBER: PCT/EP2003/010881
FRIOR FILING DATE: 2003-10-01
FRIOR PAPLICATION NUMBER: DE 10317955.0
FRIOR PILING DATE: 2003-04-17
FRIOR PILING DATE: 2003-010-07
FRIOR APPLICATION NUMBER: DE 10300096.8
FRIOR APPLICATION NUMBER: DE 10245779.4
FRIOR FILING DATE: 2003-010-07
FRIOR FILING DATE: 2002-10-01
FRIOR FILING DATE: 2002-10-01
FRIOR FILING DATE: 2002-10-01
FRIOR FILING DATE: 2002-10-01
FRIOR FILING DATE: 2002-10-01
FRIOR FILING DATE: 2002-10-01
FRIOR FILING DATE: 2002-10-01
FRIOR FILING DATE: 2002-10-01
FRIOR FILING DATE: 2002-10-01
FRIOR FILING DATE: 2002-10-01
CURRENT APPLICATION NUMBER: US/10/517,441
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 49.3%;
Matches 110; Conservative (
                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
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SCHMITT, Armin
SCHMITT, Manfred
LOOK, Maxime P.
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MODEL, Fabian
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1717 ATTTTGAAATAAGAATTAGATTTTTAAAATAAAATTTTTAAATTTTTAAATTTTTAGAT 1776
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                                                                                                                                                                                                                 ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-506-111-174
                                                                                                                                                                                                                                                                                                  Query Match 8.0%; Score 42.2; DB 6; Length 16579; Best Local Similarity 49.3%; Pred. No. 1.4; Matches 110; Conservative 0; Mismatches 113; Indels 0;
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ne : 183.849 secs
PRIOR APPLICATION NUMBER: PCT/EP03/02035 PRIOR FLILING DATE: 2003-02-27 PRIOR APPLICATION NUMBER: EP02004551.4 PRIOR FILING DATE: 2002-02-27 NUMBER POS SEQ ID NOS: 1030 SEQ ID NO 174 LENGTH: 16579
                                                                                                                                                                  TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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Publication No. US20060246433A1
Publication No. US20060246433A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Burger, Matthias
APPLICANT: Maier, Sabine
APPLICANT: Maier, Sabine
APPLICANT: Becker, Evelyne
APPLICANT: Lesche, Ralf
APPLICANT: Lesche, Ralf
APPLICANT: Lesche, Ralf
APPLICANT: Lesche, Ralf
APPLICANT: Becker, Schmitt, Armin
TITLE OF INVENTION: METHOD AND NUCLEIC ACIDS FOR THE ANALYSIS OF A COLON CELL PROLIFE
FILE REFERENCE: 47675-84/F094US
CURRENT APPLICATION NUMBER: US/10/506,111
CURRENT FILING DATE: 2004-08-27
                                                                                                                                                                                                                                                     APPLICANT: Burger, Matthias
APPLICANT: Burger, Matthias
APPLICANT: Burger, Matthias
APPLICANT: Burger, Sabine
APPLICANT: Cencrell, Susan
APPLICANT: Cotrell, Susan
APPLICANT: Cotrell, Susan
APPLICANT: Mooney, Suzanne
TITLE OF INVENTION: Method and nucleic acids for the analysis of colon cell prolifera
TITLE OF INVENTION: Misorders
FILE REFERENCE: 47675-83
CURRENT APPLICATION NUMBER: PCT/FP03/0234
PRIOR APPLICATION NUMBER: PCT/FP03/0234
PRIOR FILING DATE: 2003-02-27
PRIOR FILING DATE: 2003-02-27
PRIOR FILING DATE: 2002-02-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 8.0%; Score 42.2; DB 6; Length 16579; Best Local Similarity 49.3%; Pred. No. 1.4; Matches 110; Conservative 0; Mismatches 113; Indels 0;
                                 ATTAATTGATAATTTATAATGAAAAATATATGTTGATAATTTT 1879
         199 ATTIGICCTIAAATATATCTACAAGAAGACTTTGATATTTGT 241
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                                                                                                                                                                  Sequence 19, Application US/10506089 Publication No. US20060234224A1 GENERAL INFORMATION:
APPLICANT: Adorjan, Peter
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ORGANISM: Artificial Sequence
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LENGTH: 16579
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US-10-506-089-19
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Sequence 476, App Sequence 476, App Sequence 476, App Sequence 476, App Sequence 476, App Sequence 476, App Sequence 476, App Sequence 34190, A Sequence 438, App Sequence 475

Sequence 2, Appli Sequence 474, App Sequence 474, App Sequence 475, App Sequence 2, Appli

Sequence:

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Searched:

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THE THERAPY AND
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS OF PROSIATE CANCER
FILE REFERENCE: 210121.427C23
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                      US-11-234-786-476
US-10-357-930-13042
US-10-357-930-3813
US-10-357-930-3813
US-10-205-823-438
US-09-759-143-475
US-09-780-669-475
US-09-895-793-475
US-09-895-87-475
US-09-895-87-475
US-10-012-896-475
US-10-012-896-475
US-10-012-896-475
US-10-012-896-475
US-10-012-896-475
US-10-012-896-475
US-10-012-896-475
US-10-012-896-475
US-10-012-896-475
US-10-10-84-678A-475
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US-09-780-669-476
US-09-825-827-476
US-09-895-793-476
US-09-895-8114-476
US-10-012-896-476
US-10-010-940-476
US-10-1044-678A-476
US-10-294-025-476
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US-09-957-708-2
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US-09-780-669-474
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OTHER INFORMATION: n = A,T,C or G
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Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
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                                                                               US-09-759-143-311
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2: FBMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
3: FBMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
4: FBMC_Celerra_SIDS3/ptodata/2/pubpna/US09_PUBCOMB.seq:*
5: FBMC_Celerra_SIDS3/ptodata/2/pubpna/US108_PUBCOMB.seq:*
6: FBMC_Celerra_SIDS3/ptodata/2/pubpna/US108_PUBCOMB.seq:*
7: FBMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
8: FBMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
10: FBMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
11: FBMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
12: FBMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
13: FBMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
14: FBMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
15: FBMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
16: FBMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
16: FBMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
16: FBMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
16: FBMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
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16: FBMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
16: FBMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
17: FBMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
18: FBMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
18: FBMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
19: FBMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
10: FBMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
11: FBMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
11: FBMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
11: FBMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
11: FBMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
12: FBMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
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Sequence 21765, A
Sequence 22535, A
Sequence 27610, A
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Sequence 43052, A
Sequence 476, App
                                                                                                                                December 31, 2006, 12:22:01; Search time 837.563 Seconds (without alignments) 7716.790 Million cell updates/sec
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Sequence 311,
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Sequence 311,
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                       GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-357-930-22535
US-10-357-930-2610
US-10-357-930-28370
US-10-357-930-43052
US-10-357-930-43052
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US-09-780-669-311
US-09-232-887-311
US-09-232-880-311
US-09-895-793-311
US-10-012-896-311
US-10-010-940-311
US-10-144-678A-311
US-10-294-025-311
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                                                                                               OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum Match 100%
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Maximum DB seq length: 2000000000
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                                                                                                                        TITIGACGITITICICITAAACIACIAAAAGAGGCAITAAIGAICCAIAAAITAIATAITAICIA 120
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                                                                            1 CAAATTTGAGCCAATGACATAGAATTTTACAAAATCAAGAAGCTTATTCTGGGGCCATTTC 60
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                                                            CAAATTTGAGCCAATGACATAGAATTTTACAAATCAAGAAGCTTATTCTGGGGCCATTTC
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                             Gaps
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APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Henderson, Robert A.
APPLICANT: Retler, Marc M.
APPLICANT: Fanger, Garry R.
APPLICANT: Fanger, Garry R.
APPLICANT: Forly, John A.
APPLICANT: Carter, Darrick
APPLICANT: Vedvick, Thomas S.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Wang, Ajun
APPLICANT: Wang, Ajun
APPLICANT: Wang, Ajun
APPLICANT: Wang, Ajun
APPLICANT: Mang, Ajun
APPLICANT: Monelil, John
APPLICANT: Monelil, Patricia D.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF SEVENCE: 2001-02-09
CURRENT APPLICATION NUMBER: US/09/780,669
CURRENT APPLICATION NUMBER: US/09/780,669
CURRENT APPLICATION NUMBER: 2001-02-09
NUMBER OF SEQ ID NOS: 943
SOFTWARE: FastSEQ for Windows Version 3.0
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                             Indels
             Pred. No. 6.7e-113;
; Mismatches 0;
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Patent No. US20020051977A1
GENERAL INFORMATION:
100.08; L.
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Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
                                526; Conservative
             Similarity
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US-09-780-669-311
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Sequence 311, Application US/09822827
Sequence 311, Application US/09822827
Sequence 311, Application US/09822827
GENERAL INFORMATION:
APPLICAMT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 2010.1.534C1
CURRENT APPLICATION NUMBER: US/09/822,827
CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FASESEQ for Windows Version 3.0
SEQ ID NO 311
LENGTH: 526
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                                                                                                                                                                                                    Query Match
100.0%; Score 525; DB 3; Length 526;
Best Local Similarity 100.0%; Pred. No. 6.7e-113;
Matches 526; Conservative 0; Mismatches 0; Indels
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CCATION: (1)...(526)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                   ט
TYPE: DNA
ORGANISM: Homo sapien
FRATURE:
MAME/KEY: misc_feature
LOCATION: (1)...(526)
OTHER INFORMATION: n = A,T,C or
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ORGANISM: Homo sapien
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                                                       61 TTTTGACGTTTTCTCTAAACTACTAAAGAGGCATTAAATGATCCATAAATTATTATTATCTA
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                         TTTTGACGTTTTCTCTAAACTACTAAAGAGGCATTAATGATCCATAAATTATATTATCTA
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APPLICANT: Foy, Teresa
APPLICANT: Foy, Teresa
APPLICANT: Foy, Teresa
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
TILLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
CURRENT APPLICATION NUMBER: US/09/895,793
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 311
LENGTH: 526
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Fublication No. US2002019276341
FUBLICAUT: NTORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Carter, Marc W.
APPLICANT: Carter, Darick
APPLICANT: Carter, Darick
APPLICANT: Li, Samuel X.
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McNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
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Skeiky, Yasir A.W.
Hepler, William T.
Henderson, Robert A.
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ORGANISM: Homo sapien
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                                                                                                                         CAAATTTGAGCCAATGACATAGAATTTTACAAATCAAGAAGCTTATTCTGGGGCCATTTC
                                                                                                                                                                                             TTTTGACGTTTTCTCTAAACTACTAAAGAGGCATTAATGATCCATAAATTATATTATCTA
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US-09-132-880-311

Sequence 311, Application US/09232880

Sequence 311, Application US/09232880

Sequence 311, Application US/09232880

GENERAL INFORMATION:

APPLICANT: VAU, Jiangchun

APPLICANT: Dillon, Davin C.

APPLICANT: Mitcham, Jennifer Lynn

TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF

TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF

TITLE REFERENCE: 210121.42866

CURRENT APPLICATION NUMBER: US/09/232,880

CURRENT FILING DATE: 1999-01-15

NUMBER OF SEQ ID NOS: 338

SEQ ID NO 311

LENGTH: 526

LENGTH: 526
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100.0%; Score 525; DB 3; Length 526; 100.0%; Pred. No. 6.7e-113;
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100.0%; Score 525; DB 3; L
Best Local Similarity 100.0%; Pred. No. 6.7e-113;
Matches 526; Conservative 0; Mismatches 0;
                                             0; Mismatches
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LOCATION: (1)...(526)
OTHER INFORMATION: n = A,T,C or
                      Best Local Similarity 100.
Matches 526; Conservative
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ORGANISM: Homo sapien
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                                                                                                                                                                                                                                                                                                   Length 526;
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY ITILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER FILE REFERENCE: 210121.427026 CURRENT APPLICATION NUMBER: US/09/895,814 CURRENT FILING DATE: 2001-06-29 NUMBER OF SEQ ID NOS: 990 SOFTWARE: FASESEQ for Windows Version 3.0 SEQ ID NO 311 LENGTH: 526
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100.0%; Pred. No. 6.7e-113;
utive 0; Mismatches 0;
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APPLICANT: Dillon, Davin C.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
                                                                                                                                                                                               FEATURE:
NAME/KRY: misc_feature
LOCATION: (1)...(526)
OTHER INFORMATION: n = A,T,C or
                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 526; Conservative
                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                       ; OTHER INFORMAT
US-09-895-814-311
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US-10-012-896-311
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McNeill, Patricia D.
Houghton, Raymond L.
Vinalg de Bassols, Carlota
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Publication No. US20020193296A1
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Micham, Vagin L.
APPLICANT: Alang, Yuqiu
APPLICANT: Retter, March D.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
       ; NAME/KEY: misc_feature
; LOCATION: (1)...(226)
; OTHER INFORMATION: n = A,T,C or
US-09-895-793-311
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Hepler, William T.
Henderson, Robert A.
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Fanger, Gary R.
                                                                                         Query Match
Best Local Similarity 100.
Matches 526; Conservative
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            Sequence 311, Application US/10010940 Publication No. US20030088062A1 GENERAL INFORMATION:
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LOCATION: (1)...(526)
                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapien
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APPLICANT: Panderando, Yoshihiro
APPLICANT: Wantenando, Yoshihiro
APPLICANT: Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REPERENCE: 21011.437C27
CURRENT APPLICATION NUMBER: US/10/012,896
NUMBER OF SEQ 1D NOS: 1011
SOFTWARE: FASTESO for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 526;
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                                                                                                         MCNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: n = A,T,C or US-10-012-896-311
                                           Skeiky, Yasir A.W.
Hepler, William T.
Henderson, Robert A.
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Carter, Darrick
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Best Local Similarity 100.
Matches 526; Conservative
               , Samuel X.
                               Wang, Aijun
                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                Foy, Teresa
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LENGTH: 526
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100.0%; Score 525; DB 6; L
Best Local Similarity 100.0%; Pred. No. 6.7e-113;
Matches 526; Conservative 0; Mismatches 0;
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US-10-010-940-311
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US-10-294-025-311
; Sequence 311, Application US/10294025
; Publication No. US20030185830A1
; GENERAL INFORMATION:
; APPLICAMT: Stolk, John A.
; APPLICAMT: Kalos, Michael D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DAGNOSIS OF PROSTATE CANCER
; FILE REFREENCE: 210121.427C29
; CURRENT APPLICATION NUMBER: US/10/294,025
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 1038
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 311
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100.0%; Score 525; DB 7; L
Best Local Similarity 100.0%; Pred. No. 6.7e-113;
Matches 526; Conservative 0; Mismatches 0;
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ORGANISM: Homo sapiens
PEATURE:
NAME/KEY: misc_feature
LOCATION: 499
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APPLICANT: Watanabe, Yoshihiro
APPLICANT: Deng, Ta
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C28
CURRENT APPLICATION NUMBER: US/10/144,678A
CURRENT FILING DATE: 2002-08-12
NUMBER OF SEQ ID NOS: 1033
SOFTWARES: FASISEQ for Windows Version 3.0
SEQ ID NO 311
LENGTH: 526
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McNeill, Patricia D.
Houghton, Raymond L.
Vinals y de Bassols, Carlota
Foy, Teresa M.
Watanabe, Yoshihiro
                 Sequence 311, Application US/10144678A Publication No. US20030157089A1 GENERAL INFORMATION:
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; OTHER INFORMATION: n = A,T,C or G
US-10-144-678A-311
                                                                            APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Falos, Michael D.
APPLICANT: Falos, Michael D.
APPLICANT: Falos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Carter, Jarrick
APPLICANT: Carter, Jarrick
APPLICANT: Garter, Jarrick
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: Heyler, William T.
APPLICANT: Howlet, John
APPLICANT: Howlet, John
APPLICANT: Howleton, Raymond L.
APPLICANT: Howleton, Raymond L.
APPLICANT: Foy, Teresa M.
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                                                                    TTTTGACGTTTTCTCTAAACTACTAAAGAGGCATTAATGATCCATAAATTATATTATCTA
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; LOCATION: 1, 7, 9, 11, 1199; 1200, 1201, 1202, 1203

; CTHER INCRMATION: n = A,T,C or G

US-10-357-930-21765
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APPLICANT: Endege, Wilson
APPLICANT: Monahan, John
TITLE OF INVENTION: IDENTIFICATION, ASSESSMEN
TITLE OF INVENTION: IDENTIFICATION, ASSESSMEN
TITLE OF INVENTION: HUMAN PROSTATE CANCER
FILE REFERENCE: MXI-OO'BCN
CURRENT PELLING DATE: 2003-02-04
PRIOR PELLING DATE: 2003-02-16
PRIOR APPLICATION NUMBER: 09/785,276
PRIOR PILING DATE: 2000-01-17
PRIOR APPLICATION NUMBER: 60/183,319
PRIOR FILING DATE: 2000-03-16
PRIOR PILING DATE: 2000-03-16
PRIOR PELLING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: 60/219,454
PRIOR PILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR PILING DATE: 2000-06-09
PRIOR PILING DATE: 2000-06-09
PRIOR FILING DATE: 2000-06-09
PRIOR FILING DATE: 2000-06-09
PRIOR FILING DATE: 2000-07-18
PRIOR PILING DATE: 2000-07-18
PRIOR PILING DATE: 2000-12-13
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 21765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence 21765, Application US/10357930 ; Publication No. US20040259086A1 ; GENEAL INFORMATION: APPLICANT: Schlegel. Robert
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APPLICANT: Skeiky, Yasir A.

TITLE OF INVENTION: PROGYTHE-SPECIFIC POLYPEPTIDES AND FUSION
TITLE OF INVENTION: PROGYTHE-SPECIFIC POLYPEPTIDES AND FUSION
TITLE OF INVENTION: PROGYTHE-SPECIFIC POLYPEPTIDES AND FUSION
FILE REFERENCE: 210121.427C31
CURRENT APPLICATION NUMBER: US 09/568,857
PRIOR APPLICATION NUMBER: US 09/568,857
PRIOR FILING DATE: 2000-05-29
PRIOR FILING DATE: 2000-06-27
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: US 09/483,672
PRIOR APPLICATION NUMBER: US 09/483,672
PRIOR PILING DATE: 1999-11-12
PRIOR FILING DATE: 1999-11-12
PRIOR FILING DATE: 1999-07-13
PRIOR FILING DATE: 1999-01-15
PRIOR FILING DATE: 1999-01-15
PRIOR FILING DATE: 1999-01-15
PRIOR FILING DATE: 1999-01-15
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PRIOR FILING DATE: 1998-07-13
PRIOR FILING DATE: 1998-07-14
PRIOR PLING DATE: 1998-07-14
PRIOR PLING DATE: 1998-07-14
PRIOR PLING DATE: 1998-07-14
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SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                              Sequence 311, Application US/11234786 Publication No. US20060024301A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                      APPLICANT: Xu, Jiangchun APPLICANT: Xu, Jiangchun APPLICANT: Dillon, Davin C. APPLICANT: Mitcham, Jennifer L. APPLICANT: Harlocker, Susan L. APPLICANT: Reed, Steven G. APPLICANT: Renger, Michael D. APPLICANT: Renger, Michael D. APPLICANT: Retter, Marc W. APPLICANT: Retter, Marc W. APPLICANT: Stolk, John A. APPLICANT: Carter, John A. APPLICANT: Vedvick, Thomas S. APPLICANT: Carter, Darrick
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OTHER INFORMATION: n = A,T,C or G
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Best Local Similarity 100.
Matches 526; Conservative
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ORGANISM: Homo sapien
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LENGTH: 526
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Sequence 22535. Application US/10357930

Publication No. USCO040259086A1

GENERAL INFORMATION:
APPLICANT: Schlegel. Robert
APPLICANT: Endege, Wilson
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
TITLE OF INVENTION: UDGNIFICATION WHERE: US/10/357,930

CURRENT APPLICATION NUMBER: US/10/357,930

CURRENT FILING DATE: 2003-02-04

FRIOR FILING DATE: 2000-02-16

PRIOR FILING DATE: 2000-02-16

PRIOR FILING DATE: 2000-03-16

PRIOR FILING DATE: 2000-05-25

PRIOR FILING DATE: 2000-05-25

PRIOR FILING DATE: 2000-05-16

PRIOR FILING DATE: 2000-05-18

PRIOR FILING DATE: 2000-05-18

PRIOR FILING DATE: 2000-05-18

PRIOR FILING DATE: 2000-05-18

PRIOR FILING DATE: 2000-01-18

PRIOR FILING DATE: 2000-05-18

PRIOR FILING DATE: 2000-01-18

PRIOR PRIOR FILING DATE: 2000-01-18

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                    Length 1203;
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                      DB 9;
                    90.9%; Score 477.2; DB 9; 98.8%; Pred. No. 1.6e-101; ive 0; Mismatches 3;
             Ouery Match
Best Local Similarity 98.8
Marches 512; Conservative
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                                                                                                                          Query Match 90.9%; Score 477.2; DB 9; Best Local Similarity 98.8%; Pred. No. 1.6e-101; Matches 512; Conservative 0; Mismatches 3;
                                                               1200, 1201, 1202,
or G
TYPE: DNA

GRGANISM: Homo sapiens
FEATURE:

NAME/KEY: misc_feature

J. COCATION: 1, 7, 9, 11, 1199, 12

GTHER INFORMATION: n = A,T,C Or
US-10-357-930-22535
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Search completed: December 31, 2006, 13:56:08 Job time: 839.563 secs
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Publication No. US20040259086A1
GENERAL INFORMATION:
APPLICANT: Schlegel. Robert
APPLICANT: Endege, Wilson
APPLICANT: Monahan, John
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDEATIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
TITLE OF INVENTION: HUMAN PROSTATE CANCER
FILE REFERENCE: MRI-007BCN
CURRENT APPLICATION NUMBER: US/10/357,930
CURRENT FILING DATE: 2003-02-04
PRIOR APPLICATION NUMBER: 09/785,276
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; NAME/KEY: misc_feature
; LOCATION: 1, 7, 9, 11, 1199, 1200, 1201, 1202, 1203
; OTHER INFORMATION: n = A,T,C or G
US-10-357-930-27610
                                                                                                                                                                                                                                                                                                                Score 477.2; DB 9;
Pred. No. 1.6e-101;
0; Mismatches 3;
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 27610
; LENGTH: 1203
                                                                                                                                                                                                                                                                                                                Query Match 90.9%;
Best Local Similarity 98.8%;
Matches 512; Conservative
                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
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NAME/KEY: misc_feature

LOCATION: 1, 7, 9, 11, 1199, 1200, 1201, 1202, 1203

CTHER INFORMATION: n = A,T,C or G

US-10-357-930-28370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 477.2; DB 9;
Pred. No. 1.6e-101;
0; Mismatches 3;
PRIOR FILING DATE: 2003-02-16
PRIOR APPLICATION NUMBER: 60/183,319
PRIOR FILING DATE: 2000-02-17
PRIOR FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: 60/189,862
PRIOR FILING DATE: 2000-03-16
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-06-09
PRIOR FILING DATE: 2000-06-09
PRIOR FILING DATE: 2000-06-09
PRIOR FILING DATE: 2000-07-18
PRIOR FILING DATE: 2000-07-18
PRIOR FILING DATE: 2000-10-18
PRIOR FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 62232
SECTAMARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 98.8%;
Matches 512; Conservative
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Database

Result

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AA669621 op38g04.8
AL175696 Tetracdon
AL070972 Drosophil
AG201107 Pan trogl
AG368406 Mms muscu
AL106996 Drosophil
AL106996 Drosophil
BL069706 Drosophil
AL069706 Drosophil
AL06921 URS BAMEO94TF
AL069201 BAMEO94TF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSS 04-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AMBLISU449 684 bp DNA linear GSS 04-NOV-200 Pan troglodytes DNA, clone: PTB-142D13.F, genomic survey sequence. AG130449
BZ433986 BONNX83TF
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ban troglodytes
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
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CNS020K7
CNS00FMC
AG201107
AG368405
CNS01461
CNS0145P
DU092632
BZ563321
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iite 2 : SacI.
Location/Qualifiers
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Hominidae; Pan.
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R.Site 2
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RESULT 1
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AG093969 Pan trog1
BAG0915128 CIT-HSP-2
BAG08119 BX098119
AA643706 aj442605.8
R82378 yjlab01.r1
BE654624 PM0-BT075
AA22828 hD26407.8
BE637798 RC2-ET002
BF001177 7959010.x
AA25072 nH32h04.8
AG0802217 HS 3167
CE393091 tig7-988-AG06621 Pan trog1
AG26621 Pan trog1
AG201137 Pan trog1
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BF678216 602086120
                                                                                                                                                                      (without alignments)
6976.201 Million cell updates/sec
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                                                                                                                                             December 31, 2006, 12:14:13 ; Search time 4216.27 Seconds
                                                                                                                                                                                                                                                                          1 caaatttgagccaatgacat......tttaatccccaaagcacagt 526
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                   GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                                                                                                                                                                                                                                                                                                                                    48236798 seqs, 27959665780 residues
                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                                      - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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ORIGIN

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/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
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Homo sapiens
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Totoki, Y., Watanabe, H. and Sakaki, Y.

Direct Submission
Submitted (O2-AUG-2001) Asao Fujiyama, The Institute of Physical
submitted (D2-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimpbeseggec.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170,
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
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Pan troglodytes DNA, clone: PTB-094J13.F, genomic survey sequence.
AG093969.1 GI:16645771
GSS.
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Ban troglodytes
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                            TTTTGACGTTTTCTCTAAACTACTACTAAAGGGCATTAATGATCCATAAATTATATATCTA
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                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
Unpublished
                                                                                                      ;
;
                                                                 68.8%; Score 361.4; DB 14; Length 684; larity 97.1%; Pred. No. 6.4e-74; Conservative 0; Mismatches 11; Indels 0;
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library'
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Matches 368; Conserv
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Location/Qualifiers

FEATURES

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478 bp DNA linear GSS 09-JUN-1998 CIT-HSP-2301D2,TF CIT-HSP Homo sapiens genomic clone 2301D2, AQUI5128
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1 (bases 1 to 478)
Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K.,
Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H.,
Simon,M. and Venter,J.C.
Use of a random BAC End Sequence Database for Sequence-Ready Map
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Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
                                                                                                                                                                                                                                                                                                                                                                   120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 AAAATGGGGAAACTCTGAAGGGTTTTAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360
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                                                                                                                                                                                                                                                                                                   CAGATTTGAGCCAATGACATAGGATTCTACAAATCAAGAAGCTTAGTCTGGGGCCATTTC 401
                                                                                                                                                                                                                                                                                                                                                                                              340 CATTTACAGCATTTAAAATGTGTTCAGCATGAAATATTAGCTACAGGAGAAGCTAAAATA 281
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   220 TITITCACAAGTGAAGCATTCTTATAAAGTGTCATAAACCTTTTGGGGGAAACTCTGGG-G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 CATTTACAGCATTTAAAATGTGTTCAGCATGAAATATTAGCTACAGGGGAAGCTAAATAA
                                                                                                                                                                                                                                                                                                                                                                   61 TTTTGACGTTTTCTCTAAACTACTAAAGAGGCATTAAATGATCCATAAATTATATTATCTA
                                                                                                                                                                                                                                                             1 CAAATTTGAGCCAATGACATAGAATTTTACAAATCAAGAAGCTTATTCTGGGGCCATTTC
                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                           1;
                                                                                                                                                     Length 678;
/clone="PTB-094J13.F"
|sex="male"
|cell_type="lymphoblast"
|cell_type="lymphoblast"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Mark Adams
Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                           Indels
                                                                                                                                                     Query Match 63.8%; Score 335; DB 14;
Best Local Similarity 94.5%; Pred. No. 9.8e-68;
Matches 358; Conservative 0; Mismatches 20;
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Unpublished (1998)
Other GSSs: CIT-HSP-2301D2.TR
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Homo sapiens
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AA843706
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                171 TITITCACAAGTGAAGCATICTTATAAAGTGTCATAAAACCTTTTGGGGGAAACTCTGGG-A 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     350 TTTTGAAGTTTTTTTTAAACTACTAAAGAGACATTAATGATCCATAAATTACATTATCTA 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        290 CATTTACAGCATTTAAAATGTGTTCAGCATGAAATATTAGCTACAGGGTAAGCTAAATAA 231
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13-21
Class: BAC ends.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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BX098119 Soares placenta Nb2HP Homo sapiens cDNA clone
IMAGP998102228 ; IMAGE:149065, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 289; DB 11; Length 478;
Pred. No. 5.6e-57;
0; Mismatches 20; Indels
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                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55.0%;
llarity 93.6%;
Conservative
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Homo sapiens
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Best Local Similarity
Matches 323; Conserv
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BX098119/c
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DEFINITION
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AA843706 524 bp mRNA linear EST 31-DEC-1998
aj42£05.81 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1392993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 CAAATTTGAGCCAATGACATAGAATTTTACAAATCAAGAAGCTTATTCTGGGGC--ATTT 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       183 CTTTGACGTTTTCTCTAAACTACTAAAGAGGCATTAATGATCCATAAATATTATATTATTATTATTA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATTTACAGCATTTAAAATGTGTTCAGCATGAAATATTAGCTACAGGGGAAGCTAAATAA 180
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Tel: +49 30 32639 101

www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
M13r, Primer Sequence: TTTCACACAGGAAACAGCTATGAC.
Location/Qualifiers
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Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini,
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index (Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTTTGACGTTTTCTCTAAACTACTAAAGAGGCATTAATGATCCATAAATTATATTATCTA
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Email: cgapbs-r@mail.nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 224.2; DB 4; Length 597;
Pred. No. 8.6e-42;
0; Mismatches 3; Indels 2;
                                                                                                                                                                                                                                                                              clone="IMAGp998I02228 ; IMAGE:149065"
                                                                                                                                                                                                       organism="Homo sapiens"
                                                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA843706.1 GI:2933062
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42.7%;
Best Local Similarity 97.9%;
Matches 238; Conservative (
                                                                                                                                                                                                                                                                                                        sex="Female
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AA843706
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AUTHORS
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                                                                                                                                                                                                                                                   CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCT-CGAP clone distribution information can be
cloud through the I.M.A.G.E. Consortium/LINL at:
www-bio.llnl.gov/bbrp/limage.html
Insert Length: 948 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 474.

1. 524
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  304 CAAATTTGAGCCAATGACATAGAATTTTACAAATCAAGAAGCTTATTCTGGGGCCATTTC 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATTTACAGCATTTAAAATGTGTTTCAGCATGAAATATTAGCTACAGGGGAAGCTAAATAA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                424 CATITACAGCATITAAAAIGIGITICAGCAIGAAATAITAGCIACAGGGGAAGCIAAAIAA 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAAATTTGAGCCAATGACATAGAATTTTACAAATCAAGAAGCTTATTCTGGGGCCCATTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTTTGACGTTTTCTCTAAACTACTAAAGAGGCATTAATGATCCATAAATTATTATTATCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
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1 (bases 1 to 360)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          360 bp mRNA linear EST :
yj18b01.r1 Soares placenta Nb2HP Homo sapiens cDNA clone
IMAGE:149065 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 524;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  484 ATTAAACATGGAATAAAGATTTGTCCTTAAAAATAATCTAC 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 ATTAAACATGGAATAAAGATTTGTCCTTAAATATAAATCTAC 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ä,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 216.2; DB 1
Pred. No. 6.3e-40;
0; Mismatches 3
                                                                                                                                                                         organism="Homo sapiens"
                                                                                                                                                                                                                         clone="IMAGE:1392993"
                                                                                                                                                                                       /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 98.6%;
Matches 218; Conservative
                                                                                                                                                                                                                                           sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R82378.1 GI:861769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sapiens
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3onaldo,
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                                                                                                                                                              source
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SOURCE
ORGANISM
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JOURNAL
COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R82378/c
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/dev stage="placenta obtained at birth (full term)"
/lab_host="placenta obtained at birth (full term)"
/lab_host="DH10B (ampicillin resistant)"
/clone lib="Soares placenta Nb2HP"
/note="Organ: placenta; Vector: placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori placenta; Vectori
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1 (bases 1 to 301)

Dias Neto, B., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Madai, M.A., Baia, G.H., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST 11-SEP-2000 mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                               Source: IMAGE Consortium, LINL
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 694 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 TITGACGITITCICTAAACTACTAAAGGCATTAATGATCCATAAATTATATTATCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 AAATTTGAGCCAATGACATAGAATTTTACAAATCAAGAAGCTTATTCTGGGGCCATTTCT
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 694
High quality sequence stops: 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 10; Length 360;
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PMO-BT0757-240500-003-D01 BT0757 Homo sapiens CDNA,
BE694624
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95.1%; Pred. No. 4.8e-31;
ive 0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seg primer: M13RP1
High quality sequence stop: 238.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:9606"
/clone="IMAGE:149065"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="GDB:560899"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 95.1
Matches 195; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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JOURNAL PUBMED

COMMENT

TITLE

FEATURES

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Email: cgapbs-remail.nih.gov

Email: cgapbs-remail.nih.gov

Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui,

Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui,

M.D., Michael Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: David B. Krizman, Ph.D.

CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Context Library Arrayed hy: Genome Systems Inc., Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Context Long the I.M.A.G.E. Consortium/LINL at:

www-bio.llnl.gov/bbrp/image/fmage.html

Insert Length: 890 Std Error: 0.00

Seq primer: -40ml3 fwd. Er from Amersham

High quality sequence stopp: 325.

High quality sequence stopp: 325.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /done lib="NOI CGAP Pr3"
//done lib="NOI CGAP Pr3"
//note="Vector: PAMP10; Site_1: Not1; Site_2: EcoRI; 1st
sgrand cDNA was primed with Oilgo(dT)17 on 50 ng of
DNAse-treated, total cellular RNA obtained from
5,000-10,000 microdissectéd cells
histologically-determined to be fully malignant prostate
cancer cells. Double-stranded cDNA was ligated to EcoRI
adaptors, 5 cycles of PCR applied to the cDNA with an
adaptor-specific primer, and the resulting PCR product
subcloned into pAMP10 by the UDG-cloning method (Life
Technologies). Average insert size is 600 bp. NOTE: Not
directionally cloned. This library was constructed by
David Krizman."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BE827798 22-SEP-2000 RC2-ET0022-170500-015-all ET0022 Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 448 ITCCCTTTTTAGTATCTGTGTATCAAGTATAAAAGTTCTATAAACTGTAGTNTACTTATT 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  374 ATACAGAAATGAGTGGCTGAGATTCTTGATTGCATAGC-AGAGCTTCTCATCTAAACCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      328 AGTATCTTACCTGAAGCTACAGACTCCATAACCTCTTTTACAGGGAGCTCCTGCAGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           434 AGTGGGTTCCCTGAAGCTACAGACTCCATAACCTCTTTTAGAGGGAGCTCCTGCAGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 388 CTACAGAAATGAGTGGCTGAGATTCTTGATTGCACAGCAAGAGCTTCTCATCTAAACCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 145.2; DB 1;
Pred. No. 2.6e-23;
0; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /dev_stage="45 years old"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapier
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:953485"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tch 27.7%; al Similarity 91.6%; 175; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="Male"
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1 (bases 1 to 288)
                          Unpublished (1997)
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Best Local Similarity
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                                JOURNAL
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BE827798
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                                                                                                                                                                                                                                                                                                                                      Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=PM0-BT0757-240
Seq primer: puc 18 forward
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mkNA"
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/de_regge="Adult"
/clone=lib=BT0557"
/note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65 AACCTCTTTTACAAAGAGCTCCTGCAGCTCCTACAGAAATGAGTGGCTGAGATTTCTTGA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGCACAGCAAGAGCTICTCAICTAAACCCTITCCCTITITAGIAICTGIGIATCAAGIA 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGCATAGC-AGAGCTICTCATCCAAACCCTITCCCTTTTAGTGTCTGTGTATC-AGTA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64
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Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                   Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                          Shotgun sequencing of the human transcriptome with ORF expressed
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1 (bases 1 to 462)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       297 GGAAAAAATGGGGAAACTCTGAAGGGTTTTAAGTATCTTACCTGAAGCTACAGACTCCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 GGAGAAAATGGAGAAACTCTGAAGGGTTTTAAGTACCTTTCCTGAAGCTGCAGACTCCAT
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                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
10737800
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93.2%; Pred. No. 2.2e-28;
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/organism="Homo sapiens"
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AA528286.1 GI:2270355
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                                                                                 sequence tags
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Query Match

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417 125

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183

RESULT 8 AA528286/c DEFINITION VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

REFERENCE AUTHORS TITLE

387 375 447 316

Gaps

5

(CGAP)

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/clone lib="NCI CGAP_Pr28"
/note="Cogan: prostate; Vector: pT773D-Paci; Plasmid DNA from the normalized library NCI CGAP Pr22 was prepared, and st circles were made in vitro. Pollowing HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 985608-986759, 1101192-1101959, and 117928-11220615). Subtraction by Bento Soares and M. Patima Bonaldo. "
                                                                                                                                                                                                    Email: cgapbe-remail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing Dy: Washington University Genome Sequencing Center
DNA Sequencing Dy: Washington University Genome Sequencing Center
Clone distribution: NI-CGAP Cone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 432.
High quality sequence stop: 432.
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nh32h04.s1 NCI_CGAP_Pr3 Homo sapiens CDNA clone IMAGE:954103, mRNA
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini;
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
1 (Bases 1 to 554)
1 (Bases 1 to 554)
NOI-(CAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CC
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Pred. No. 4.6e-23;
0; Mismatches 3;
                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
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/clone="IMAGE:3310770"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="adult"
/lab_host="DH10B"
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ilarity 96.8%;
Conservative
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Unpublished (1997)
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Best Local Similarity
Matches 179; Conserv
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                                                                                      AUTHORS
                                                                                                                                                           JOURNAL
                                                             REFERENCE
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                                                                                                             TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                         Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
This asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC2-ET0022-170
500-015-all&t3=2000-05-17&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 17
High quality sequence stop: 288.
Location/Qualifiers
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          Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTTTAGTATCTGTGTATCAAGTATAAAAGTTCTATAAACTGTAGTNTACTTATTTTAATC 513
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Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                                 Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                           Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              334 TTACCTGAAGCTACAGACTCCATAACCTCTTTACAGGGAGCTCCTGCAGCCCCTACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  394 AAATGAGTGAGATTCTTGATTGCACAGCAAGAGCTTCTCATCTAAACCCTTTCCCT
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                                                                                                                                                                                                               Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27.5%; Score 144.2; DB 7
96.8%; Pred. No. 4.3e-23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'organism="Homo sapiens"
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                                                                                                                                                                                                                                                               Contact: Simpson A.J.G.
                                                                                                                                                                                                                                                                                                                                                                                       rel: +55-11-2704922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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BF001177
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10737800
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BF001177
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Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NISC gj11g01.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3271488 CB049577
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         553 CCTGAAGATGCAGACTCCATAACCTCTTTACANAGAGCTCNTGCAGCTCATACAGAGA 494
                                                                                                                                                                                          High Throughput Sequencing Center
University of Mashington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3818
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 3167 row: H column: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 457 TAGTATCTGTGTATCAAGTATAAAAGTTCTATAAACTGTAGTNTACTTATTTAATCCC 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          434 TAGTGTCTGTGTATC-AGTATAAAAGTTCTATAAACTGTGTAGT-TACTTATTTAATCCC 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                 Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999) 10449764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  493 TGAGTGGCTGAGATTCTTGATAGCATAGC-AGAGCTTCTCATCCAAACCCTTTCCCTTNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   397 TGAGTGGCTGAGATTCTTGATTGCACAGGAGGCTTCTCATCTAAAACCCTTTCCCTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1997)
Contact: Nobert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
CDNA Library Preparation:
CDNA Library Preparation:
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC)
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F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="genomic_DNA"
/db_xref="taxon:9606"
/clone="Plate=3167 Col=22 Row=H"
                                                                                                                                                                      Contact: Mahairas GG, Wallace JC, Hood L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23.6%; Score 124; DB 11;
91.1%; Pred. No. 2.5e-18;
iive 0; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stop: 559.
Location/Qualifiers
1.,559
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 91.1
Matches 163; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: T7
Class: BAC ends
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CB049577
       AUTHORS
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone lib="NGI_CGAP Pr3"
//clone lib="NGI_CGAP Pr3"
//otoe="Vector: pAMPJ0; Site_1: Not1; Site_2: EcoRI; 1st
strand cDNA was primed with Oilgo(dT)17 on 50 ng of
DNAse-treated, total cellular RNA obtained from
5,000-10,000 microdissected cells
histologically-determined to be fully malignant prostate
cancer cells. Double-stranded cDNA was ligated to EcoRI
adaptors, 5 cycles of PCR applied to the cDNA with an
adaptor-specific primer, and the resulting PCR product
subcloned into pAMPIO by the UDG-cloning method (Life
Technologies). Average insert size is 600 bp. NOTE: Not
directionally cloned. This library was constructed by
                                                                                                                                     Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui,
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui,
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Genome Systems Inc., Gree Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40ml3 fwd. ET from Amersham.
Location/Qualifiers
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HS_3167_B2_D11_T7C_CIT_Approved Human Genomic Sperm Library D Homo
Rapiens genomic clone Plate=3167_Col=22_Row=H, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTACCTGAAGCTACAGACTCCATAACCTCTTTACAGGGAGCTCCTGCAGGCCCCTACAG 393
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 559)
                         1 (bases 1 to 265)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       146 TTACCTGAAGCTACAGACTCCATAACCTCTTTACAGGGAGCTCCTGCAGCCCCTACAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24.2%; Score 126.8; DB 1; 97.9%; Pred. No. 5e-19; rative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="45 years old"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:954103"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTTTAGTATCTGTGTATCAAGT 475
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AQ802217
AQ802217.1 GI:5719549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sex="Male"
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Homo sapiens
                                                                                                  Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 24.2
Best Local Similarity 97.9
Matches 139; Conservative
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AQ802217/c
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Gaps

435

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21.1%; Score 110.6; DB 12; 73.1%; Pred. No. 3.3e-15; tive 0; Mismatches 59;
                                                                      organism="Canis familiaris"
                  shotgun.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pan troglodytes (chimpanzee)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : pKS145
: SacI
: SacI
Email: ekirknes@tigr.org
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LIBRARY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               232 TGATATTTGTTTT 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 709)
                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 TAATATTTGTTT 1
                                                     1. 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pan troglodytes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vector
R.Site 1
R.Site 2
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Best Local Similarity
Matches 185; Conserv
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                  Class:
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                                                       Rourge
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AG056621
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                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                /clone lib="NCI CGAP_Pr28"
/note="Organ: prostate; Vector: pT773D-PacI; Plasmid DNA from the normalized library NCI CGAP_Pr22 was prepared, and ss circles were made in vitro. FOllowing HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR camplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDS 985608-986759, 1101192-1101959, and III P17928-1220615). Subtraction by Bento Soares and M.
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov Plate: LLAM8008 zvw: N column: 1 Seq primer: -21M13 forward primer (ABI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Kirkness BF
The Institute for Genomic Research
Department of Bukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0208
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tigr-gss-dog-17000334478329 Dog Library Canis familiaris genomic, genomic, survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             334 TTACCTGAAGCTACAGACTCCATAACCTCTTTACAGGGAGCTCCTGCAGCCCCTACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   394 AAATGAGTGGCTGAGATTCTTGATTGCACAGCAAGAGCTTCTCATCTAAACCCTTTCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAATGAGTGGCTGAAATTTTTGATTGCACAACAA-AACTTTTCATCTAAACCCTTTCCCT
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Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
Venter,J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The dog genome: survey sequencing and comparative analysis Science 301 (5641), 1898-1903 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4; Length 577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23.3%; Score 122.4; DB 4
89.7%; Pred. No. 5.9e-18;
iive 0; Mismatches 16
                                                                                                          1. :577
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:3271488"
                                                                                                                                                                                                                  dev stage="adult"
|ab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                    Patima Bonaldo
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CE393091.1 GI:36634243
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Canis familiaris
                                                                                                                                                                                                   sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Canis.
1 (bases 1 to 434)
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Matches 165; Conservative
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Losdes I to 703, W., Toyoda.A., Taylor,T.D., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
Submitted (Oz-NUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@spc.riken.go.jp, URL.http://hgp.gsc.riken.go.jp/, Tel:sla 145-5203-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                           ω
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          193 CTTTTTAAGTTCTTTCTAAGCTACTCAAGAGGCAACTGGTTCTCCATAAATTATATCATC 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGUSE621 709 bp DNA linear GSS 02-NOV-200:
Pan troglodytes DNA, clone: PTB-042P10.F, genomic survey sequence.
AG056621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 TACATTTACAGCATT-----TAAAATGTGTTCAGCATGAAATATTAGCTACAGGGGAA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCTAAATAAATTAAACATGGAATAAAGATTTGTCCTTAAATATAATCTACAAGAAGACTT 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            253 CAAACTTGAGTTAATGGCACAGAATTTTACAAGATCAAAAAGCTTCATCTAGAGCATTT 194
                                                                                                                                                                                                                                                                                                                                                                                                             59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTTTTGACGTTTTCTCTAAAGTACTAAAGAGGC-ATTAATGATCCATAAATTATATC
                                                                                                                                                                                                                                                                                                                                                                                                                 1 CAAATTTGAGCCAATGACATAGAATTTTACAA-ATCAAGAAGCTTATTCTGGGGCCATTT
                                                                                                                                                                                                                                                                                                                                           Gaps
/moi_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="texon:9615"
/clone_lib="Dog_Library"
/note="Site_1: BstXI; Libraries were prepared from peripheral blood"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
Unpublished
                                                                                                                                                                                                                                                                                                                                               6
                                                                                                                                                                                                                                                                                DB 12; Length 434;
                                                                                                                                                                                                                                                                                                                                           Indels
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